

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2004, 19:49:24 ; Search time 3021 Seconds
(without alignments)
3791.690 Million cell updates/sec

Title: US-09-513-365A-1

Perfect score: 1481

Sequence: 1 MLGQQQQQLYSALLTGER.....DNEKTMDSKSTKTKDRRSR 280

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlp
-Q/cn2_1/USPTO_spool_p/US09513365/runat_12012004_163932_28772/app.query.fasta_1.455
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-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -NORM SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09513365 @CN 1.1 4958 @runat_12012004_163932_28772 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1481	100.0	840	6	AR213554	AR213554 Sequence
2	1481	100.0	1078	6	AR213555	AR213555 Sequence
3	1481	100.0	1078	9	AB012853	AB012853 Homo sapi
4	1481	100.0	1080	6	AX211560	AX211560 Sequence
5	1481	100.0	1080	9	AF053537	AF053537 Homo sapi
6	1481	100.0	1141	9	BC030128	BC030128 Homo sapi
7	1478	99.8	843	9	HSAG6851	AJ006851 Homo sapi
8	1422.5	96.0	1262	10	BC050003	BC050003 Mus muscu
9	1399.5	94.5	1001	10	AF078834	AF078834 Mus muscu
10	1334	90.1	1154	6	AR220840	AR220840 Sequence
11	1197	80.8	974	9	HSING282	AF062748 Homo sapi
12	1197	80.8	18317	9	AC107214	AC107214 Homo sapi
13	1157	78.1	192753	2	AC107236	AC107236 Mus muscu
14	1152	77.8	231311	2	AC129666	AC129666 Rattus no
15	1152	77.8	245104	2	AC128348	AC128348 Rattus no
16	1152	77.8	247796	2	AC094539	AC094539 Rattus no
17	1152	77.8	255408	2	AC129658	AC129658 Rattus no
18	1041	70.3	1094	5	AY014017	AY014017 Xenopus l
19	1008	68.1	42029	2	AC114762	AC114762 Homo sapi
20	962	65.0	666	4	AB098919	AB098919 Bos tauru
21	880.5	59.5	840	10	AF149820	AF149820 Mus muscu
22	874.5	59.0	1584	10	BC016573	BC016573 Mus muscu
23	874.5	59.0	2817	10	AF177757	AF177757 Mus muscu
24	853.5	57.6	840	9	AF078835	AF078835 Homo sapi
25	853.5	57.6	845	9	HSAG10392	AJ310392 Homo sapi
26	853.5	57.6	873	6	AR171884	AR171884 Sequence
27	853.5	57.6	911	9	AF044076	AF044076 Homo sapi
28	853.5	57.6	1533	6	AX367042	AX367042 Sequence
29	853.5	57.6	1533	9	AF149721	AF149721 Homo sapi
30	853.5	57.6	2444	9	AB024401	AB024401 Homo sapi
31	853.5	57.6	2897	9	AF181850	AF181850 Homo sapi
32	750	50.6	1944	10	AF177756	AF177756 Mus muscu
33	750	50.6	1959	10	AF177755	AF177755 Mus muscu
34	749	50.6	184918	2	AC114608	AC114608 Mus muscu
35	749	50.6	235079	2	AC124475	AC124475 Mus muscu
36	748	50.5	201302	2	AC120896	AC120896 Rattus no
37	748	50.5	222955	2	AC135534	AC135534 Rattus no
38	733.5	49.5	888	9	AB037594	AB037594 Homo sapi
39	730	49.3	1074	9	AF149722	AF149722 Homo sapi
40	728	49.2	1143	6	AX367043	AX367043 Sequence
41	728	49.2	1189	9	AF149723	AF149723 Homo sapi
42	728	49.2	1902	6	AR079046	AR079046 Sequence
43	728	49.2	1902	6	AR087457	AR087457 Sequence
44	728	49.2	1902	6	AR110646	AR110646 Sequence
45	728	49.2	1902	6	AR154563	AR154563 Sequence

ALIGNMENTS

RESULT 1

AR213554 AR213554 840 bp DNA linear PAT 25-SEP-2002
LOCUS Sequence 6 from patent US 6403785.
ACCESSION AR213554
VERSION AR213554.1 GI:23310821
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE Unclassified.
AUTHORS Nagata,M., Ozaki,K., Shimada,Y. and Horie,M.
TITLE Isolated DNA molecule encoding human TSC403
JOURNAL Patent: US 6403785-A 6 11-JUN-2002;
FEATURES Location/Qualifiers
source
1..840
BASE COUNT 297 a 164 c 211 g 168 t
ORIGIN
Alignment Scores:
Pred. No.: 1.39e-113 Length: 840
Score: 1481.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 1 MetLeuGlyGlnGlnGlnGlnLeuTyrSerSerAlaLeuLeuThrGlyGluArg 20
DB 1 ATGTTAGGCGCAGCAGCAGCACTGTACTCGCGCGCGCTCTGACCGGGAGCGG 60
QY 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40
DB 61 AGCGCGCTGCTCACTGCTACGTGCGAGGACTACCTTGAGTGGGTGGAGTGGCGCCAC 120
QY 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
DB 121 GACATGCAGAGGAACGTGCTGTGCTGCGAGAGCTGGACAACAAATATCAAGAAACGTTA 180
QY 61 LysGluLeuAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
DB 181 AGGAAATTTGATGATGCTACGAAATATAGAAAGAGATGATTTAAACCAAGAGAAA 240
QY 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGlnLeuGlyAspGluLys 100
DB 241 CGTCTACAGCAGCTTCTCCAGAGAGCCTAAATTAATAGTCAAGAAATGGGAGATGAAAA 300
QY 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120
DB 301 ATACAGATTTTACACAAATGCTCGAATTTGGTGGAAAAATCGGGCAAGACAAATGGAGTTA 360
QY 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
DB 361 CACTCACAGTGTTCACAGATCTCTGCTGAAGTGAACGAGCTCAGATTAAGCAAGATG 420
QY 141 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 160
DB 421 GATTCAGCAACCAAGAGATCTTCAAGAAAGACCCCGCAGCGAGCGAGTGAAGC 480
QY 161 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGlu 180
DB 481 CTGTGATTTATGTCATATGCAATGGGATTTGAAGACTGTGATGATCAGCCACTTAAGAA 540
QY 181 LysLysSerLysSerAlaLysLysLysArgSerLysAlaLysGlnGlnArgGluAla 200
DB 541 AGAAATCCAGTACGCAAGAGAAACAAACGCTCCAGGCCACGACGGAAGGGAGCT 600
QY 201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal 220
DB 601 TCACCTGTTGAGTTTGCATATAGATCTTAATGAACCTTACATACTGCTTATGCAACCAAGT 660

QY 221 SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe 240
DB 661 TCTTATGGGAGATGATAGGATGTGACAAATGAACAGTGTCCAATGAATGGTTTCACTTT 720
QY 241 SerCysValSerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGly 260
DB 721 TCATGTGTTTCACTTACCTATAAACCAAGGGGAAATGTTATGGCCCAAGTGCAGGGGA 780
QY 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSerArg 280
DB 781 GATAATGAGAAACAATGCAAAAGTACTGAAAAAGACAAAAAGATAGAAATCGAGG 840
RESULT 2
AR213555 AR213555 1078 bp DNA linear PAT 25-SEP-2002
LOCUS Sequence 7 from patent US 6403785.
ACCESSION AR213555
VERSION AR213555.1 GI:23310822
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE Unclassified.
AUTHORS Nagata,M., Ozaki,K., Shimada,Y. and Horie,M.
TITLE Isolated DNA molecule encoding human TSC403
JOURNAL Patent: US 6403785-A 7 11-JUN-2002;
FEATURES Location/Qualifiers
source
1..1078
BASE COUNT 356 a 206 c 280 g 236 t
ORIGIN
Alignment Scores:
Pred. No.: 1.92e-113 Length: 1078
Score: 1481.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-513-365A-1 (1-280) x AR213555 (1-1078)
QY 1 MetLeuGlyGlnGlnGlnGlnLeuTyrSerSerAlaLeuLeuThrGlyGluArg 20
DB 92 ATGTTAGGCGCAGCAGCAGCACTGTACTCGCGCGCGCTCTGACCGGGAGCGG 151
QY 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40
DB 152 AGCGCGCTGCTCACTGCTACGTGCGAGGACTACCTTGAGTGGGTGGAGTGGCGCCAC 211
QY 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
DB 212 GACATGCAGAGGAACGTGCTGTGCTGCGAGAGCTGGACAACAAATATCAAGAAACGTTA 271
QY 61 LysGluLeuAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
DB 272 AAGAAATTTGATGATGCTACGAAATATAGAAAGAGATGATTTAAACCAAGAGAAA 331
QY 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGlnLeuGlyAspGluLys 100
DB 332 CGTCTACAGCAGCTTCTCCAGAGAGCCTAATTAATAGTCAAGAAATGGGAGATGAAAA 391
QY 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120
DB 392 ATACAGATTTTACACAAATGCTCGAATTTGGTGGAAAAATCGGGCAAGACAAATGGAGTTA 451
QY 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
DB 452 CACTCACAGTGTTCCTCAAGATCTCTGCTGAAGTGAACGAGCTCAGATTAAGCAAGATG 511
QY 141 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 160
DB 512 GATTCAGCCCAACCAAGAGATCTTCAAGAAAGACCCCGCAGCGAGCGAGTGAAGC 571

QY 161 ArgAspLeuCysHisMetAlaHsnGlyIleGluAspCysAspAspGlnProProLysGlu 180
 Db 572 CGTGATTATGTGACATGGCAATGGATTGAAGACTGTGATGATCAGCCACCTAAAGAA 631

QY 181 LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla 200
 Db 632 AAGAAATCCAACTCAGCAAGAAAGAAACGCTCCAAGGCCCAAGCAAGGAAAGGAAGCT 691

QY 201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal 220
 Db 692 TCACCTGTGTGAGTTGGCAATAGATCTCTAATGAACCTACATCTGCTTATGCAACCAAGTG 751

QY 221 SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe 240
 Db 752 TCTTATGGGAGATGATAGTGTGACAAATGAACAGTGTCCAATGAATGGTTTTCACITT 811

QY 241 SerCysValSerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGly 260
 Db 812 TCATGTGTTTCACTTACCTATTAAACCAAGGGGAAATGGTATTGCCCAAGTGCAGGGGA 871

QY 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSerArg 280
 Db 872 GATAATGAGAAACAATGCAAAAGTACTGAAAGACAAAAGATAGAAAGATCGAGG 931

RESULT 3

AB012853 1078 bp mRNA linear PRI 18-MAR-1999
 LOCUS Homo sapiens INGL1 mRNA for INGL1p, complete cds.

DEFINITION

AB012853

ACCESSION

AB012853.1 GI:4115554

VERSION

INGL1p.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (sites)

AUTHORS

Shimada,Y., Saito,A., Suzuki,M., Takahashi,E. and Horie,M.

TITLE

Cloning of a novel gene (INGL1) homologous to INGL1, a candidate

JOURNAL

tumor suppressor

MEDLINE

Cytogenet. Cell Genet. 83 (3-4), 232-235 (1998)

PUBMED

99172097

REFERENCE

2 (bases 1 to 1078)

AUTHORS

Shimada,Y., Saito,A. and Horie,M.

TITLE

Direct Submission

JOURNAL

Submitted (07-APR-1998) Yoshikazu Shimada, Otsuka Pharmaceutical

Co. Ltd., Otsuka GEN Research Institute, Kagasuno, Kawauchi-cho,

Tokushima, Tokushima 771-0192, Japan

(E-mail:shim@otsuka.genome.ad.jp, Tel:81-886-65-2888(ex.2476),

Fax:81-886-37-1035)

Sequence updated (17-Apr-1998).

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="4"

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/dev_stage="fetal"

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92..934

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RDLCHMANGIEDDDPPKPKSKAKKKRSKAKQEREASPVFAIDPNEPTYCLCN

QVSYGEMIGCDNEQCPIEFHFSCVSLTYKPKGKWKYCPKCRGDNEKTMWDKSTKTKKD
 RRSr"

BASE COUNT 356 a 206 c 280 g 236 t

ORIGIN

Alignment Scores:

Pred. No.: 1.92e-113 Length: 1078
 Score: 1481.00 Matches: 280
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-513-365A-1 (1-280) x AB012853 (1-1078)

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 Db 92 ATGTTAGGGCAGCAGCAGCAACTGCTCGCGCGCGCTCTGACCGGGAGCGG 151

QY 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValIcuSerLeuProHis 40
 Db 152 AGCCGGCTGCTCACCTGCTACGTGCGAGACTACCTTGAGTGGTGGAGTGGCTGCCAC 211

QY 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
 Db 212 GACATGCAGAGCAACGCTGCTGCTGCGAGAGCTGGACCAACAAATATCAAGAAACGTTA 271

QY 61 LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
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QY 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlnGluGlyAspGluLys 100
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QY 101 IleGlnIleValThrGlnMetLeuGluValGluAsnArgAlaArgGlnMetGluLeu 120
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QY 121 HisSerGlnCysPheGlnAspProGluSerGluArgAlaSerAspLysAlaLysMet 140
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 Db 512 GATTCACCCCAACCAAGAAAGATCTTCAAGAGACCCCGCAGCAGCGGACCACTGAAGC 571

QY 161 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGlu 180
 Db 572 CGTGATTATGTCAATGGCAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAA 631

QY 181 LysLysSerLysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAla 200
 Db 632 AAGAAATCCAAAGTCAAGCAAGAAAGAAAGCGCTCAAGGGCCAGCAGAGGGAAGCT 691

QY 201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal 220
 Db 692 TCACCTGTGTGAGTTTGCATAGATCTAATGAACCTACATCTGCTTATGCAACCAAGTG 751

QY 221 SerTyrGlyGluMetIleGlyCysAspAsnGlnGlnCysProIleGluTrpPheHisPhe 240
 Db 752 TCTTATGGGAGATGATAGGATGTGACAAATGACAGTGTCCAATTTGAATGGTTTTCATT 811

QY 241 SerCysValSerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGly 260
 Db 812 TCATGTGTTTTCATTACCTATTAACCAAGGGGAAATGGTATTTGCCAAAGTGCAGGGGA 871

QY 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSerArg 280
 Db 872 GATAATGAGAAACAATGCAAAAGTACTGAAAGACAAAAGATAGAAAGATCGAGG 931

RESULT 4

AX211560


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Db      601 TCACCTGTTGAGTTTGCATAGATCTTAATGAACCTACATACCTGCTTATGCAACCAAGTG 660
QY      221 SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe 240
Db      661 TCTTATGGGAGATGATAGATGTGACATGACATGACATGCTCCATTAATGTTTCACTTT 720
QY      241 SerCysValSerLeuThrTyrIlysProLysGlyGlyTyrTyrCysProLysCysArgGly 260
Db      721 TCATGTGTTTCACTTACCTATAAACCAAGGGGAAATGGTATTGCCAAAGTCAGGGGA 780
QY      261 AspAsnGluLysThrMetAspLysSerThrGluLysThrIlysLysAspArgSerArg 280
Db      781 GATAATGAGAAAAACAATGGCAAAAGTACTGAAAAAGCAAAAAAGGATGAGATCGAGG 840

RESULT 8
BC050003
LOCUS   1262 bp mRNA linear ROD 01-APR-2003
DEFINITION Mus musculus, similar to inhibitor of growth family, member 1-like,
clone IMAGE:6515125, mRNA, partial cds.
ACCESSION BC050003
VERSION   BC050003
KEYWORDS  BC050003.1 GI:29436709
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     1 (bases 1 to 1262)
JOURNAL   Strausberg, R.
DIRECT SUBMISSION
Submitted (31-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gcgaps@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hgrl.nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Teurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 108 Row: 0 Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 12963706.
Location/Qualifiers
1. .1262
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/strain="FVB/N-3"
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old mouse. Taken by biopsy."
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/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6"
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/codon_start=1
CDS

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1-like"
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SRDLCHMTNGIDDCDDQPPKEXRSKAKKRSKAKQERASPVFAIDPNPFTYCLC
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BASE COUNT 320 a 310 c 422 g 210 t
ORIGIN
Alignment Scores:
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Score: 1422.50 Matches: 269
Percent Similarity: 98.21% Conservatives: 5
Best Local Similarity: 96.42% Mismatches: 4
Query Match: 96.05% Indels: 1
DB: 10 Gaps: 1
US-09-513-365A-1 (1-280) x BC050003 (1-1262)
QY 1 MetLeuGly---GlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGlu 19
Db 425 ATGTTAGGCGCAGCAGCAGCAGCAGCTGTACTCGTCGCCGCGCTCTCGACCGGAGAG 484
QY 20 ArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuPro 39
Db 485 CGGAGCGCGCTCTCACCTGCTACCTGTCAGGAGTACTACCTGGAGTGTGTGGAGTCGCC 544
QY 40 HisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThr 59
Db 545 CACGACATGCAGAGAGACGTGTCGGTGTCTGGGAGCTGGACACACAAATCCAGAAACG 604
QY 60 LeuLysGluIleValThrGlnMetLeuGluValGluAsnArgAlaArgGlnMetGlu 119
Db 605 TTAAGGAAATTTGATGATGCTCTATGAAAAATATAAGAAAGAGATGATTCACACAGAAA 664
QY 80 LysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGlnLeuGlyAspGlu 99
Db 665 AAACCCCTACAGCAGCATCTCCAGAGAGCGTTTAATCAATAGCAAGAATTTGGAGATGAA 724
QY 100 LysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGlu 119
Db 725 AAAATTGAGATTGTCCACGAGATGCTCGAATTTGGTGGAGACCGAGCAGACAAATGGAG 784
QY 120 LeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLys 139
Db 785 CTGCATTACAGCTGTTTCAGGATCTCTGCTGAAGTGAGCGAGCTTCAGCAAGTCGAAG 844
QY 140 MetAspSerSerGlnProGluArgSerSerArgArgProArgGlnArgThrSerGlu 159
Db 845 ATGGATTCCAGTCAACCGGAAAGATCTTCTAGAAGACCTTCGAAGACAGAGGAGGAG 904
QY 160 SerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspGlnProProLys 179
Db 905 ACCCGTGACTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 964
QY 180 GluLysLysSerLysSerAlaLysLysLysLysLysLysLysLysLysLysLysLys 199
Db 965 GAAAGAGATCCAACTCCGCCAAGAAAGAGAGCGCTCCAGGCCAAGCAGGAGGAGGAG 1024
QY 200 AlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGln 219
Db 1025 GCATCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
QY 220 ValSerTyrGlyGluMetIleGlyCysAspAsnGlnGlnCysProIleGluTrpPheHis 239
Db 1085 GTGTCCTACGGGAGATGATGAGCTGTGACATGAAACAGTGTCCCATGTAATGGTTTAC 1144
QY 240 PheSerCysValSerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArg 259

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Db 1145 TTTTCATGTGTTTCACTACCTATATAACCAACCGGGAATGGTATTGTCCTCAAAAGTGAGG 1204
Qy 260 GlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArg 278
Db 1205 GGGAGACAATGAGAAAAACCATGGACAAAAGTACCGAAAAGACAAAAAAGAAAAA 1261

RESULT 9
AF078834
LOCUS AF078834 1001 bp mRNA linear ROD 09-SEP-2000
DEFINITION Mus musculus p33ING2 (Ing2) mRNA, complete cds.
ACCESSION AF078834
VERSION AF078834.1 GI:10039542
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1001)
Nagashima,M., Hagiwara,K., Hancock,A.R. and Harris,C.C.
Direct Submission
Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, National Institutes of Health, 37
Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA
FEATURES
Location/Qualifiers
1..1001
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/mol_type="mRNA"
/db_xref="taxon:10090"
1..1001
/genes="Ing2"
8..853
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/codon_start=1
/product="p33ING2"
/protein_id="AAG12173.1"
/db_xref="GI:10039543"
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ERROR"
BASE COUNT 324 a 205 c 264 g 208 t
ORIGIN
Alignment Scores:
Pred. No.: 9,49e-107 Length: 1001
Score: 1399.50 Matches: 266
Percent Similarity: 97.15% Conservative: 7
Best Local Similarity: 94.66% Mismatches: 7
Query Match: 94.50% Indels: 1
DB: 10 Gaps: 1

US-09-513-365A-1 (1-280) x AF078834 (1-1001)
Qy 1 MetLeuGly---GlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuThrGlyGlu 19
Db 8 ATGTTAGGCGAGCAGCAGCAGCAGCAGCTGCTCTGCGCGCGCTCTCTGACCGGAGAG 67
Qy 20 ArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuPro 39
Db 68 CGGAGCGCGCTGCTACCTGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
Qy 40 HisAspMetGlnArgSerValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThr 59
Db 128 CACGACATGCAGAGGAACGTGCTCGGTGCTCGCGAGCTGCACAAACAAATACCAAGAAACG 187
Qy 60 LeuLysGluLeuAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLys 79
Db 188 TTAAGGAAATTCATGATGCTATGAAAAATATGAGAAAGAGAGATGATTCACCAACCAAGAA 247
Qy 80 LysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGlnLeuGlyAspGlu 99
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Db 248 AAACGCCTACAGCAGCATCTCCAGAGAGCGTTAATCAATAGTAAAGAAATGGGAGATGAA 307
Qy 100 LysIleGlnIleValThrGlnMetLeuGluLeuValGluLeuAsnArgAlaArgGlnMetGlu 119
Db 308 AAAATTCAAGATGTCACCCAGATGCTCGGATTGGTGGAGAACCGATCGAGACAAATGGAG 367
Qy 120 LeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLys 139
Db 368 CTGCATTACAGTGTTCCTCAGGATCTGCTGAAAGTGGAGCGAGCTCAGACAAGTCGAAG 427
Qy 140 MetAspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGlu 159
Db 428 ATGGATTCCAGTCAACCGGAAAGATCTTCTAGAACCTCGAAGACAGACAGGACCAAGTGA 487
Qy 160 SerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProLys 179
Db 488 AGCCCTGATCTTATGTCATGACAAACCGGATTGACGACTGTGATGATCAACCCGAAA 547
Qy 180 GluLysLysSerLysSerAlaLysLysLysLysLysLysLysLysLysLysLysLysLys 199
Db 548 GAAAGAGATCCAAAGTCCGCCAAGAAAGAGCGCTCCAGGCCCAAGCAGGAGGAG 607
Qy 200 AlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGln 219
Db 608 GCATCCTCTGTCGAGTTTGCCATCGATCCCAATGAGCCCACTACTGCTTGTGTAACCAA 667
Qy 220 ValSerTyrGlyGluMetIleGlyCysAspAsnGlnGlnCysProIleGluThrPheHis 239
Db 668 GTGCTCTACGGGAGATGATAGGCTGTGACATGAACAGTGTCCCATGAAATGGTTTAC 727
Qy 240 PheSerCysValSerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArg 259
Db 728 TTTTCATGTGTTTCACTCACTATATAACACAGGGGAAATGGTATTGCCCAAGTGAAG 787
Qy 260 GlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSer 279
Db 788 GGAGACAATGAGAAACCATGACAAAAGTACCGAAAAGACAAAAAAGGAGAGAGAGCG 847
Qy 280 Arg 280
Db 848 AGG 850

RESULT 10
AR220840
LOCUS AR220840 1154 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 81 from patent US 6426186.
ACCESSION AR220840
VERSION AR220840.1 GI:23327717
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1154)
AUTHORS Jones,K.A., Volkuth,W. and Walker,M.G.
TITLE Bone remodeling genes
JOURNAL Patent: US 6426186-A 81 30-JUL-2002;
FEATURES location/Qualifiers
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/organism="unknown"
BASE COUNT 367 a 216 c 285 g 265 t 21 others
ORIGIN
Alignment Scores:
Pred. No.: 2,95e-101 Length: 1154
Score: 1334.00 Matches: 270
Percent Similarity: 81.87% Conservative: 1
Best Local Similarity: 81.57% Mismatches: 9
Query Match: 90.07% Indels: 53
DB: 6 Gaps: 1

US-09-513-365A-1 (1-280) x AR220840 (1-1154)
Qy 1 MetLeuGlyGlnGlnGlnGlnLeuTyrSerSerAlaLeuThrGlyGluArg 20
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QY 112 GluAspArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSer 131
 DB |||||
 DB 285 GAAATCGGCAAGACAAATGAGTTACACTCACAGTGTTCACAGATCTCTGCTGAACT 344
 QY 132 GluArgAlaSerAspLysAlaLysMetAspSerGlnProGluArgSerArgArg 151
 DB |||||
 DB 345 GAACGAGCCTCAGATAAAGCAAGATGGATTCCAGGCCAACCCAGAAAGATCTTCAAGAAGA 404
 QY 152 ProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGlu 171
 DB |||||
 DB 405 CCCCAGCAGCAGCGGACCAAGTGAAGCCGTGATTTATGTACATGCCAATGGGATGAA 464
 QY 172 AspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLysLysLysArg 191
 DB |||||
 DB 465 GACTGTGATGATCAGCCACTAAAGAAAGAAATCCAGTCAGCAAGAAAGAAAGAACGC 524
 QY 192 SerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGlu 211
 DB |||||
 DB 525 TCCAGGCCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTGCAATAGATCTCAATGAA 584
 QY 212 ProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGlu 231
 DB |||||
 DB 585 CCTACATACCTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGCAATGAA 644
 QY 232 GlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGly 251
 DB |||||
 DB 645 CAGTGTCCAATTGAATGGTTTCACTTTTCAATGTTTCACTTACCTATTAAACCAAGGGG 704
 QY 252 LysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGlu 271
 DB |||||
 DB 705 AAATGCTATTGCCAAAGTGCAGGGGAGATAATGAGAAACCAATGACAAAGATGACTGAA 764
 QY 272 LysThrLysLysAspArgSerArg 280
 DB |||||
 DB 765 AAGACAAAAAGATAGAAGATCGAGG 791

RESULT 12
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 LOCUS Homo sapiens BAC clone RP11-367N14 from 4, complete sequence.
 DEFINITION AC107214
 ACCESSION AC107214.5 GI:23238103
 VERSION HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 183317)
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074
 REFERENCE 2 (bases 1 to 183317)
 AUTHORS Nguyen, C., Haglund, K. and Spalding, L.
 TITLE The sequence of Homo sapiens BAC clone RP11-367N14
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 183317)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (16-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 183317)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (10-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 183317)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2002) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 6 (bases 1 to 183317)
 Waterston, R.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@watson.wustl.edu
 Summary Statistics
 Center project name: H_NH0367N14

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AC112698.

There is an unresolved tandem repeat from base 87660 to 89441.

Data from AC112698 was used to finish this clone.

FEATURES

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 856..1214
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 2782..3132
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repeat_region	4643..4762	/rpt_family="Alu"
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repeat_region	14111..14206	/rpt_family="L1"
repeat_region	14565..14864	/rpt_family="Alu"
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repeat_region	19348..19529	/rpt_family="Alu"
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repeat_region	23182..23212	/rpt_family="(TAAA)n"

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Best Local Similarity:	92.77%	Mismatches:	9
Query Match:	80.82%	Indels:	6
DB:	9	Gaps:	2

US-09-513-365A-1 (1-280) x AC107214 (1-183317)			
QY	32	LeuGluCysValGluSerLeuProHisAspMetGlnArgAsnValSerValLeuArgGlu	51
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QY	52	LeuAspAsnLysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLys	71
DB	45200	CTT-----TTTTTAGAAACGTTAAAGGAAATTTGATGATGTCTACGAAAAATATAAG	45250
QY	72	LysGluAspAspLeuAsnGlnLysLysArgLeuGlnGlnLeuGlnArgAlaLeuIle	91
DB	45251	AAAGAAGATGATTTTAAACCAGAGAAACGCTTACAGCAGCTTCTCCAGAGAGCCTAATT	45310
QY	92	AsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuVal	111
DB	45311	AATAGTCAAGAAATTCGGAGATGAAAAAATACAGATTGTTTACACAAATGCTCGAATTGGTG	45370
QY	112	GluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSer	131
DB	45371	GAATAATCGGGCAAGACAAATGGAGTTTACACTCACAGTGTGTTCCAGATGCTGCTGAAGT	45430
QY	132	GluArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerArgArg	151
DB	45431	GAACGAGCCTCAGATAAAGCAAGATGGATTTCAGCCAAACCGAAAGATCTTCAAGAAGA	45490
QY	152	ProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGlu	171
DB	45491	CCCCGAGCGCAGCGGACCAAGTGAAGCCGCTGATTATGTACATGTCACAAATGGGATTGAA	45550
QY	172	AspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLysLysLysArg	191
DB	45551	GACTGTGATGATCAGCCACCTAAAGAAAAAGAAATCCCAAGTCAGCAAGAAAAAGAAACGC	45610
QY	192	SerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGlu	211
DB	45611	TCCAAGGCCCAAGCAGAAAGGGAAGCTTCCACCTGTTGAGTTTGCAATAGATCTTAATGAA	45670
QY	212	ProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGlu	231
DB	45671	CCTACATACTGCTTATGCAACCAAGTGCTTTATGGGAGATGATAGATGTGACATGAA	45730
QY	232	GlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGly	251
DB	45731	CAGTGTCCAATGAATGGTTTCACTTTTCATGTGTTTCACTTACCTATTAACCAAGGGG	45790

ORIGIN

Alignment Scores: 9.21e-84 Length: 192753
 Pred. No.: 1157.00 Matches: 215
 Score: 1157.00 Conserves: 6
 Percent Similarity: 98.22% Mismatches: 4
 Best Local Similarity: 95.56% Indels: 0
 Query Match: 78.12% Gaps: 0
 DB: 2

US-09-513-365A-1 (1-280) x AC107236 (1-192753)

QY 56 TyrGlnGluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspAsp 75
 ::
 Db 98076 TTTTGAACACGTTAAAGGAAATTCATGTCTATCAAAAATATAAGAAAGAGATGAT 98017

QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuLeuSerGlnGlu 95
 ::
 Db 98016 TCCAAACGAGAAAACCGCTACAGCAGCATCTCCAGAGACGCTTAATCAATAGCCCAAGAA 97957

QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
 ::
 Db 97956 TTGGGAGTGAATAATTCAGATGTCACCCAGATGCTCGAATGTGGAGAACCGAGCG 97897

QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSer 135
 ::
 Db 97896 AGACAAATGAGCTGCATTCACAGTGTTCACAGATCCTCTAGAAAGTGCAGGCTCA 97837

QY 136 AspLysAlaLysMetAspSerSerGlnProGluArgSerSerArgProArgArgGln 155
 ::
 Db 97836 GACAAGTCGAGAGATGATTCAGTCAACCGGAAGATCTTCTAGAAAGCTCCAGACAG 97777

QY 156 ArgThrSerGluSerArgAspLeuGluHisMetAlaAsnGlyIleGluAspCysAspAsp 175
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 Db 97776 AGACCACTGAGAGCGTGTGATTCATGACATGACAAACGGGATTCAGCACTGTGATGAT 97717

QY 176 GlnProLysGluLysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLys 195
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 Db 97716 CAACCCGAGAAAGAGATCCAGTCCGCCCAAGAGAGAGCGCTCCAGGCCAAG 97657

QY 196 GlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCys 215
 ::
 Db 97656 CAGGAGAGGAGGAGCATCCCTGTCGATTTGCCATCGATCCCAATGAGCCCACTACTGC 97597

QY 216 LeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIle 235
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 Db 97596 TTGTGTAAACCAAGTGTCTACGGGGAGATGATAGGCTGTGACATGACAGTGTCCCAT 97537

QY 236 GluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTyrTyrCys 255
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 Db 97536 GAATGTTTCATCTTTTCATGTGTTTCACTCACTATTAACCCAGGGGAATGTATTCG 97477

QY 256 ProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLys 275
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 Db 97476 CCAAGGTGAGGGAGACATGAGAAACCATGACAAAGATGCCGAAAGACAAAGAAAG 97417

QY 276 AspArgArgSerArg 280
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 Db 97416 GAGAGAAGACGAGG 97402

RESULT 14
 AC132966/c
 LOCUS Rattus norvegicus clone CH230-210B24, WORKING DRAFT SEQUENCE, 2
 DEFINITION Rattus norvegicus clone CH230-210B24, WORKING DRAFT SEQUENCE, 2
 unnumbered pieces.
 AC132966
 AC132966.4 GI:25073360
 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus; Chordata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 231311)
 Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Faves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hoques, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensu, L., Loulseghe, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Frankoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D., Sneed, A., Sodargren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlaczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

TITLE
JOURNAL

2 (bases 1 to 231311)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (05-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 231311)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS

3 (bases 1 to 231311)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 COMMENT
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence


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QY 176 GlnProProLysGluLysLysSerLysSerAlaLysLysLysLysLysLysLysLysLysLys 195
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QY 196 GlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCys 215
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Db 110657 TTATGTAAACCAAGTGCTTTACGGGGAGATGATAGGCTGTGACAATGAACAGTGTCCCAAT 110598

QY 236 GluTTPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCys 255
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QY 256 ProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLys 275
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QY 276 AspArgArgSerArg 280
Db 110477 GAGAGAAGAGCGAGG 110463
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Search completed: January 12, 2004, 22:12:19
Job time : 3230 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2004, 17:23:57 ; Search time 268 Seconds
(without alignments)
2820.308 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1481	100.0	840	20	AAZ08595	Human INGL encodi
2	1481	100.0	1078	20	AAZ08596	Human INGL encodi
3	1481	100.0	1080	22	AAZ12783	Tumour suppressor
4	1345	90.8	1153	21	AAZ47473	Human tumour suppr
5	1334	90.1	1154	24	ABS70424	Human bone remodel
6	874.5	59.0	2817	21	AAAS3790	Murine P37ING1 cod
7	853.5	57.6	911	21	AAAS3792	Human P37ING1 codi
8	853.5	57.6	1533	22	AAH28478	Nucleotide sequenc
9	853.5	57.6	2897	24	ABK86977	Human inhibitor of
10	745	50.3	1835	21	AAAS3789	Murine ingl common
11	728	49.2	1143	22	AAH28479	Nucleotide sequenc
12	728	49.2	1902	18	AAT69651	Tumour suppressor
13	728	49.2	1902	19	AAV62285	Partial INGL parti
14	728	49.2	1905	24	AAZ46126	Human tumour suppr
15	728	49.2	2061	18	AAT69652	Tumour suppressor
16	728	49.2	2061	19	AAV62292	Human INGL full-le
17	728	49.2	2061	20	AAZ28688	Nucleotide sequenc
18	728	49.2	2886	24	ABK86976	Human inhibitor of
19	728	49.2	8487	22	AAI37089	Human musculoskele
20	728	49.2	8487	25	ABX60077	cDNA encoding nove
21	728	49.2	163350	24	AAZ46127	Human tumour suppr
22	604	40.8	742	22	AAH28480	Nucleotide sequenc
23	602	40.6	857	22	AAH28481	Nucleotide sequenc
24	572	38.6	346	21	AAC28459	Human secreted pro
25	480	32.4	693	24	ABO50058	Oligonucleotide fo
26	480	32.4	693	24	ABO50059	Oligonucleotide fo
27	466	31.5	693	24	ABQ50060	Oligonucleotide fo
28	466	31.5	693	24	ABQ50061	Oligonucleotide fo
29	445	30.7	1705	22	AAK51611	Human polynucleoti
30	449	30.3	1082	25	ABQ77429	Human CGDD cDNA 72
31	447	30.2	1772	23	ABL12805	Drosophila melanog
32	447	30.2	1781	21	AAAS3979	p33 tumour suppress
33	446.5	30.1	1465	21	AAAI5008	cDNA encoding a hu
34	446.5	30.1	1611	22	ABA09175	Human tumour suppr
35	446.5	30.1	1611	22	AAK52595	Human polynucleoti
36	436.5	29.5	987	23	ABL15055	Drosophila melanog
37	432.5	29.2	1365	24	ABL54076	Human tumour suppr
38	427.5	28.9	1108	22	AAF90399	Cell cycle protein
39	424.5	28.7	958	22	AAF90402	Cell cycle protein
40	424.5	28.7	1300	24	ABZ11521	Human polynucleoti
41	406	27.4	1465	22	AAK52101	Human polynucleoti
42	400	27.0	699	21	AAZ27422	IkappaB kinase (IK
43	396.5	26.8	678	21	AAZ27423	IkappaB kinase (IK
44	392.5	26.5	807	22	AAF90400	Cell cycle protein
45	392.5	26.5	807	22	AAF90401	Cell cycle protein

ALIGNMENTS

RESULT 1
AAZ08595
ID AAZ08595 standard; cDNA; 840 BP.
XX AAZ08595;
XX AC
XX AAZ08595;
DT 18-OCT-1999 (first entry)
XX
XX Human INGL encoding cDNA.
DE
DE Human; TSC403; INGL; diagnosis; lung cancer; cell cycle; regulation;
KW cell proliferation; cell aging; apoptosis; tumour suppressor; ss.
XX
XX Homo sapiens.
XX
XX Key
XX Location/Qualifiers
FT CDS
FT 1..840

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PD      12-AUG-1999.
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PF      02-FEB-1999; 99WO-JP00419.
XX
PR      28-APR-1998; 98JP-0134679.
PR      03-FEB-1998; 98JP-0038133.
PR      05-MAR-1998; 98JP-0073234.
XX
PA      (SAKA ) OTSUKA PHARM CO LTD.
XX
PI      Horie M, Nagata M, Ozaki K, Shimada Y;
XX
DR      WPI; 1999-494294/41.
DR      P-PSDB; AAY29606.
XX
PT      Human lung-specific gene TSC430 overexpressed in cancer tissue, used
PT      for treatment of, e.g. colon tumour
XX
PS      Claim 14; Page 91; 99pp; Japanese.
XX
CC      The present sequence represents the human tumour suppressor gene INGIL.
CC      The present invention also describes the human gene TSC403 expressed
CC      specifically in normal lung tissue. TSC403 is useful in the
CC      diagnosis, investigation and treatment of cancers in which it is
CC      overexpressed, including cancer of the lung, breast, fallopian tube,
CC      oesophagus, colon, thyroid, parotid gland, bladder, ovary or pancreas.
CC      INGIL is useful in the investigation of cell proliferation, aging and
CC      apoptosis and the pathology of cancer, the diagnosis and treatment of
CC      cancer such as cancer of the colon, stomach, oesophagus or fallopian
CC      tube, and the screening of candidate drugs for the treatment of such
CC      cancers.
XX
SQ      Sequence 840 BP; 297 A; 164 C; 211 G; 168 T; 0 other;

Alignment Scores:
Pred. No.:      6.16e-133      Length:      840
Score:          1481.00      Matches:      280
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:            20      Gaps:        0

US-09-513-365A-1 (1-280) x AAZ08595 (1-840)

QY      1 MetLeuGlyGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg 20
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QY      21 SerArgLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40
Db      61 AGCCGGCTGCTACCTGCTACGTCAGGACCTACTTGGAGTGGCTGCGTCCGCCAC 120

QY      41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
Db      121 GACATGCAGAGGAACGTGCTGTGCTGCGAGAGCTGGACACAAATATCAAGAAACGTTA 180

QY      61 LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
Db      181 AAGGAAATTCATGATGCTACGAAAAATATAAGAAAGAAAGATGATTTAAACCAAGAGAAA 240

QY      81 ArgLeuGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100
Db      241 CGTCTACAGCAGCTTCTTCAGAGAGCAGCAATTAATAGTCAAGAAATGGGAGATGAAA 300

QY      101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120
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QY      121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
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QY      141 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 160
Db      421 GATTCCAGCCCAACCAAGAAAGATCTTCAAGAAGACCCCGCAGCGAGCCAGTGAAGAGC 480

QY      161 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspGlnProProLysGlu 180
Db      481 CGTGATTTATGTGCATGCGCAATGGGATTGAAGACTGTGTGATGATCAGCCACCTAAAGAA 540

QY      181 LysLysSerLysSerAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLys 200
Db      541 AAGAAATCCAGTCAGCAAGAAAGAAACCTCAAGCCCAAGCAAGAAAGAGGAGCT 600

QY      201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal 220
Db      601 TCACCTGTTGAGTTTGAATAGATCTTAATGAACCTACATACCTGCTTATGCAACCAAGTG 660

QY      221 SerTyrGlyGluMetIleGlyCysAspAsnGlnGlnCysProIleGluThrPheHisPhe 240
Db      661 TCTTATGGGGAGATGATAGGATGTGACCAATGAACAGTGTCCAATGGAATGGTTTCACTTT 720

QY      241 SerCysValSerLeuThrTyrLysProLysGlyLysLysLysLysLysLysLysLysLys 260
Db      721 TCATGTGTTTCACTTACCTATTAACCAAGGGGAAATGTTATGTTCCCAANGTCAGGGGA 780

QY      261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg 280
Db      781 GATATGAGAAACAAATGGCAAAAGTACTGAAAGACAAAGAGGATAGAGATCGAGG 840

RESULT 2
AAZ08596
ID      AAZ08596 standard; cDNA; 1078 BP.
XX
AC      AAZ08596;
XX
DT      18-OCT-1999 (first entry)
XX
DE      Human INGIL encoding cDNA with 5' and 3' untranslated regions.
XX
KW      Human; TSC403; INGIL; diagnosis; lung cancer; cell cycle; regulation;
KW      cell proliferation; cell aging; apoptosis; tumour suppressor; ss.
XX
OS      Homo sapiens.
XX
FH      Key
FT      CDS
FT      92..934
FT      /*tag= a
FT      /product= "INGIL"
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PN      WO9940190-A1.
PD      12-AUG-1999.
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PF      02-FEB-1999; 99WO-JP00419.
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PR      28-APR-1998; 98JP-0134679.
PR      03-FEB-1998; 98JP-0038133.
PR      05-MAR-1998; 98JP-0073234.
XX
PA      (SAKA ) OTSUKA PHARM CO LTD.
XX
PI      Horie M, Nagata M, Ozaki K, Shimada Y;
XX
DR      WPI; 1999-494294/41.
DR      P-PSDB; AAY29606.
XX
PT      Human lung-specific gene TSC430 overexpressed in cancer tissue, used
PT      for treatment of, e.g. colon tumour
XX

```

PS Claim 15; Page 91-93; 99pp; Japanese.

XX The present sequence represents the human tumour suppressor gene INGL1.
 CC The present invention also describes the human gene TSC403 expressed
 CC specifically in normal lung tissue. TSC403 is useful in the
 CC diagnosis, investigation and treatment of cancers in which it is
 CC overexpressed, including cancer of the lung, breast, fallopian tube,
 CC oesophagus, colon, thyroid, parotid gland, bladder, ovary or pancreas.
 CC INGL1 is useful in the investigation of cell proliferation, aging and
 CC apoptosis and the pathology of cancer, the diagnosis and treatment of
 CC cancer such as cancer of the colon, stomach, oesophagus or fallopian
 CC tube, and the screening of candidate drugs for the treatment of such
 CC cancers.

XX SQ Sequence 1078 BP; 356 A; 206 C; 280 G; 236 T; 0 other;

Alignment Scores:

Pred. No.:	8,55e-133	Length:	1078
Score:	1481.00	Matches:	280
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-513-365A-1 (1-280) x AA208596 (1-1078)

QY	1	MetLeuGlyGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuThrGlyGluArg	20
Db	92	ATGTTAGGCGAGCAGCAGCAGCAACTGTACTGTCGGCGCGCTCTCTGACCGGGAGCGG	151
QY	21	SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis	40
Db	152	AGCGCGCTGCTACCTGCTACGTGCAGGACTACCTTGTAGTGGTGGAGTCGTGCCCCAC	211
QY	41	AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu	60
Db	212	GACATGCAGAGGAACGTGCTGTGCTGCGAGAGCTGGCAACAATATCAAGAAACGTTA	271
QY	61	LysGluLeuLeuAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys	80
Db	272	AGGAATTTGATGATGCTTACGNAANAATATAGAAAGAGAGATGATTTAAACCGAAGAAA	331
QY	81	ArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGlnLeuGlyAspGluLys	100
Db	332	CGTCTACAGCAGCTTCTCCAGAGAGCACAATTAATAGTCAAGAAITGGGAGATGAAAA	391
QY	101	IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu	120
Db	392	ATACAGATTGTTACACAAATGCTCGAATTTGGTGGAAAAATCGGGCAAGACAAATGGAGTTA	451
QY	121	HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet	140
Db	452	CACCTCAGTGTGTTCCAGATCTCTGCTGAAGTGAACGAGCCCTCAGATAAGCAAAAGTG	511
QY	141	AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer	160
Db	512	GATTCCAGCAACCAAGAGATCTTCAAGAGAGACCCCGCAGGAGCGGACCATGGAAGC	571
QY	161	ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGlu	180
Db	572	CGTGATTATTGTCACATGCGCAATGGGATTTGAAGACTGTGATGATCAGCCACCTAAAGAA	631
QY	181	LysLeuSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla	200
Db	632	AGAAATCCAAAGTCAGCAAGAAAAAGAACGCTCCAGGCCCAAGCAGAAAGGGAGCT	691
QY	201	SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal	220
Db	692	TCACCTGTTGAGTTTGCATAGATCTCTATGAACCTACATACTGCTTATGCACACCAAGTG	751
QY	221	SerTyrGlyGlnMetIleGlyCysAspAsnGlnGlnCysProIleGluTrpPheHisPhe	240
Db	752	TCTTATGGGAGATGATAGATGTGACAAATGAACAGTGTCCAAATTCGAATGGTTTCTACTTT	811

QY	241	SerCysValSerLeuThrTyrLysProLysGlyLysTyrTrpTyrCysProLysCysArgGly	260
Db	812	TCATGTGTTTCACTTACCTATATAACCAAGGGGAAATGGTATTGCCCAAGTCAGGGGA	871
QY	261	AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSerArg	280
Db	872	GATAATGAGAAACAATGACAAAAAGTACTGAAAAAGACAAAAAAGGATAGAAAGATCGAGG	931

RESULT 3

AAID12783
 ID AAD12783 standard; DNA; 1080 BP.

XX AAD12783;

XX AC AAD12783;

XX DT 23-OCT-2001 (first entry)

XX DE Tumour suppressor homologue protein, p33ING2 DNA.

XX KW Tumour suppressor; p47ING3; cell proliferation; cellular aging; p33ING2;
 XX KW anchorage dependence; apoptosis; tumour; cancer; gene therapy; ds.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT CDS 68..910

FT FT /*tag= a

FT FT /product= "Tumour suppressor homologue protein, p33ING2"

XX PN WO200159114-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US04425.

XX PR 09-FEB-2000; 2000US-0181292.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Harris CC, Nagashima M;

XX DR WPI; 2001-488975/53.

XX XX P-PSDB; AAE06675.

XX PT New tumor suppressor protein p47ING3 for the diagnosis and treatment of
 XX tumors -

XX PS Disclosure; Page 78; 80pp; English.

XX CC The present sequence is a DNA encoding tumour suppressor homologue
 CC protein, p33ING2 which is homologous to human tumour suppressor protein,
 CC p47ING3. The tumour suppressors of the invention are involved in the
 CC regulation of cell proliferation and in the control of cellular aging,
 CC anchorage dependence and apoptosis. The tumour suppressor protein,
 CC p47ING3, nucleic acids encoding it and antibodies against it are useful
 CC for diagnosis, prevention and treatment of tumours and cancers. The
 CC p47ING3 DNA is also used in gene therapy.

XX SQ Sequence 1080 BP; 375 A; 196 C; 271 G; 238 T; 0 other;

Alignment Scores:

Pred. No.:	8,57e-133	Length:	1080
Score:	1481.00	Matches:	280
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-513-365A-1 (1-280) x AAD12783 (1-1080)

QY	1	MetLeuGlyGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuThrGlyGluArg	20
Db	68	ATGTTAGGCGAGCAGCAGCAGCAACTGTACTGTCGGTGGCTCTCTGACCGGGAGCGG	127

Db	367	AGAAAGAGATGATTTTAAACAGAGAAAACGCTCTACAGCAGCTTCTCCAGAGAGACACTA	426
Qy	91	IleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeu	110
Db	427	ATTAATAGTCAAGAATTGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTG	486
Qy	111	ValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu	130
Db	487	GTGGAATAATCGGGCAAGCAAAATGAGATTACACTCAGCTGTTTCCAAAGATCCTGCTGAA	546
Qy	131	SerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerArg	150
Db	547	AGTGAACGAGCTTCAGATAACCAAGAAGATGATTCCAGCCAACCCAGAAAGATCTTCAAGA	606
Qy	151	ArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIle	170
Db	607	AGACCCCGCAGCGAGCGGACCACTGAAAGCGTGATTTATGTGCATGGCAAAATGGGATT	666
Qy	171	GluAspCysAspAspGlnProProLysGluLysSerLysSerAlaLysLysLysLys	190
Db	667	GAAGACTGTGATGATCAGCCACTTAAGAAAGAAGAAATCCCAAGTCAGCAAGAAAAAGAA	726
Qy	191	ArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAsn	210
Db	727	CGCTCCAAGCCNACGAGAAAGGAGAGCTTCACCTGTTGAGTTTGCATAATGATCTTAAT	786
Qy	211	GluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsn	230
Db	787	GAACCTTACATACTGCTTTATGCAACCAAGTGCTTTATGGGAGATGATAGGATGTGCAAT	846
Qy	231	GluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLys	250
Db	847	GAACAGTGTCCAAATTTGAATGGTTTTCACCTTTTCATGTGTTTACCTTAATAACCAAG	906
Qy	251	GlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThr	270
Db	907	GGGAATGGTATTGCCCAAGATGTCAGGGGAGATTAATGAGAAACAATGGACAAAGTACT	966
Qy	271	GluLysThrLysLysAspArgSerArg	280
Db	967	GAAGAACAATAAAGGATAGAGATCGAGG	996

RESULT 5

ABS70424
ID ABS70424 standard; cDNA; 1154 BP;

AC ABS70424;

27-NOV-2002 (first entry)

Human bone remodelling gene #81.

XX Bone remodelling; osteoporosis; human; gene; ss.
KW

OS Homo sapiens.

XX PN US6426186-B1.

30-JUL-2002.

18-JAN-2000: 2000US-0484970.

AA
PR 18-JAN-2000; 2000US-0484970.

PA (INCY-) INCYTE GENOMICS INC.

XX PI Jones KA, Volkmuth W, Walker MG:

AA
DR
WPI; 2002-673014/72.

A combination of polynucleotides which are co-expressed with genes known to be involved in bone remodeling and osteoporosis are useful in an array for the diagnosis of bone remodeling and osteoporosis

associated disorders -
Claim 1; Column 239-342; 206pp; English.
The invention relates to a combination comprising a number of substantially purified and isolated polynucleotides which co-expressed with genes known to be involved in bone remodelling or osteoporosis. The invention is used to diagnose disorders associated with bone remodelling or osteoporosis. ABS70344-ABS70351
human bone remodelling genes of the invention.

Sequence 1154 BP; 367 A; 216 C; 285 G; 265 T; 21 other:

Alignment Scores:

Pred. No.:	1,23e-118	Length:	1,154
Score:	1334.00	Matches:	270
Percent Similarity:	81.87%	Conservative:	1
Best Local Similarity:	81.57%	Mismatches:	9
Query Match:	90.07%	Indels:	53
DB:	24	Gaps:	1

US-09-513-365A-1 (1-280) x ABS70424 (1-1154)

Qy	1	MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg	20
Db	9	ATGTTAGNNNNNNNNNNNNNNNNNNNNCTCGTCGGCTCGCTCCTACCGGGAGCG	68
Qy	21	SerArgLeuLeuThrCysTyxValGlnAspTyrLeuGluCysValGluSerLeuProHis	40
Db	69	AC-CGGCTGCTCACCTGCTACGTCGAGCACTACCTTGAGTGGCTGGAGTCGTCGCCAC	127
Qy	41	AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyxGln	57
Db	128	GACATGACAGAGAACTGCTGTGTCTGCAGA-CTGGACAACAATATCAAGGTCGGGC	186
Qy	57	-----	57
Db	187	TGTGCCGGGGCGTTGGTTTCGGCCCCCAGCGGAGTCCGAATCGGGGTTTCAGCATGTTTT	246
Qy	57	-----	57
Db	247	CGCGTGATGTTTCCAACTCTTCCAGTCAATGGATCAGGACGGCGATCAGCAGCTCG	306
Qy	58	-----GluThrLeuLysGluLeuLeuAspValTyxGluLysTy	70
Db	307	ACCGTCGGGATCTCTGGCTCCGCAACCGCTTAAAGGAAATTTGATGATGTCTACGAAAAATA	366
Qy	70	rLysLysGluAspAspLeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLe	90
Db	367	TAAAGAAAGATGATTTAAACCAAGAAAGAAACGCTACAGCAGCTTCTCCAGAGCAGCT	426
Qy	90	uileAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLe	110
Db	427	AAITTAATAGTCAAGATTTGGAGATGAATAATACAGATTTGTACACAATGCTCGAAT	486
Qy	110	uValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaG	130
Db	487	GGTGGAAAAATCGGCAAGACAAAATGGAGTTACACTCACAGTGTTCCTCAAGATCTCTGA	546
Qy	130	uSerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerAr	150
Db	547	AAGTGAACGAGCCTCAGATAAGCAAGATGGATTCAGCCCAACACAGAAAGATCTTCAAG	606
Qy	150	gAtqProArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyL	170
Db	607	AAGACCCCGCAGCGAGCGGACCGTGAAGCCGTTATTTATGTTCATGGCAATGGGAT	666
Qy	170	eGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLysLysLysL	190
Db	667	TGAAGACTGTGATGATCAGCCACCTTAAAGAAAGAAATCCAGTCAGCAAGAAAGAA	726
Qy	190	sArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAs	210

Db 727 ACCTCAAGCCCAAGCAGGAAGGAGCTTACCTGTTGAGTTTGCATATGATCCTAA 786
 Qy 210 nGluProThrTyrCysLeuGlnValSerTyrGlyGluMetIleGlyCysAspAs 230
 Db 787 TGAACCTACATACCTGCTTATGCAACCAAGTCTTATGGGAGATGATAGGATGTGACAA 846
 Qy 230 nGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyrIlyProLy 250
 Db 847 TGAACAGTGTCCAAATGATGGTTTCATTTTCATGTGTTTCACTTACCTATAAACCAAA 906
 Qy 250 sGlyLysTyrTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerTh 270
 Db 907 GGGGAAATGATATTGCCAAAGTGCAGGGGAGAGATAATGAGAAACAATGCAAAAAGTAC 966
 Qy 270 rGluLysThrLysLysAspArgSerArg 280
 Db 967 TGAAGAGACAAAAGAGTAGAAGATCGAGG 997

RESULT 6

AAA53790
 ID AAA53790 standard; cDNA; 2817 BP.

AC AAA53790;

XX 19-DEC-2000 (first entry)

XX Murine P37ING1 coding sequence.

XX p53; tumour; cancer; detection; antibody; hybridisation; exon 1b;
 KW ING1; ing1; p37ING1; p37ING1; oncogene; gene therapy; diagnosis;
 KW proliferation disorder; transformation; transformed cell; mouse; ds.
 XX Mus musculus.

XX Key

PH Location/Qualifiers

FT CDS 847..1686

FT /*tag= a

FT /product= P37ING1 polypeptide

XX WO200046370-A1.

XX 10-AUG-2000.

XX 04-FEB-2000; 2000WO-US02959.

XX 04-FEB-1999; 99US-0118941.

XX (UNII) UNIV ILLINOIS FOUND.

XX Gudkov A, Zeremski M, Gurova KV, Grigorian IA;

XX WPI; 2000-491278/43.

XX P-PSDB; AAY97242.

XX Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing
 PT and treating cancer, comprises contacting sample with isolated nucleic
 PT acid comprising sequence of exon 1b and detecting hybridized products
 XX Disclosure; Fig 11; 134pp; English.

XX Mutations in or loss of the p53 gene occur in more than 50% of
 CC human tumours and tumour cell lines, but functional inactivation of
 CC the p53 pathway occurs in a much larger proportion of tumours. In
 CC many cases the mechanism of functional inactivation of the p53 gene
 CC remains unknown but p53 has been found to act in cooperation with
 CC ING1. Functional cooperation between ING1 and p53 suggested that
 CC ING1 encoded a tumour suppressor protein that functioned within the
 CC p53 pathway. This data suggested a possible role for ING1 in head
 CC and neck cancers and chromosomal location of the ING1 placed it
 CC within a region that is frequently rearranged in head and neck
 CC cancers. Large scale analysis of tumours involving ING1 has not
 CC revealed mutations in ING1 nor significant variations in its
 CC expression suggesting that ING1 was not a useful gene to study in

CC cancer etiology. However, alternative initiation exons of the ing1
 CC gene, each having their own promoter have been discovered.
 CC Expression of one promoter (1a) produces a protein identical to
 CC ING1. Expression of a second promoter (1b) produces a protein having
 CC an identical C-terminal fragment to ING1 but an additional 104
 CC N-terminal amino acids. The newly discovered protein has been
 CC designated p37ING1 (wild type: p37ING1). p37ING1 has the
 CC characteristics of an oncogene. When overexpressed in cells (even
 CC those expressing wild type p53) p37ING1 is able to cause
 CC proliferation or transformation of those cells. Thus detecting a
 CC nucleic acid encoding exon 1b of ing1 by hybridisation with an
 CC isolated nucleic acid having the sequence of exon 1b of ing1
 CC or its antisense sequence can identify individuals expressing the
 CC oncogenic form of ing1. Novel peptide sequences taken from the 104
 CC N-terminal peptide of p37ING1 can also be used to raise antibodies
 CC that can also be used in detection methods for the p37ING1 variant.
 CC The polypeptides may be useful in gene therapy for treatment of cell
 CC proliferation disorders, especially cancers and for diagnosing and
 CC studying cancers.

XX SQ Sequence 2817 BP; 670 A; 711 C; 846 G; 590 T; 0 other;

Alignment Scores:

Pred. No.: 5,46e-74 Length: 2817
 Score: 874.50 Matches: 165
 Percent Similarity: 77.41% Conservative: 44
 Best Local Similarity: 61.11% Mismatches: 50
 Query Match: 59.05% Indels: 11
 DB: 21 Gaps: 3

US-09-513-365A-1 (1-280) x AAA53790 (1-2817)

Qy 18 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer 37
 Db 865 GGGGAGCAGATCCACCTCGTGAAC---TATGGGAGGATTACTCGAGCTCAATCGAGTCA 921
 Qy 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
 Db 922 CTGCTTTTCGACCTCGAGGAGGACGCTCTGCTGATCGGGGAGATCGACGCCAATACCAA 981
 Qy 58 GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspLeuAen 77
 Db 982 GAGATCCTTGAAGAGCTGACGACGACTATATGAGAAAGTTCAACGGGAGACAGACGCCACC 1041
 Qy 78 GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly 97
 Db 1042 CAGAAAGCCCGGGTACTGCACCTGCATCCAGAGGGCCCTGATCCGAGCAGGAGCTAGGC 1101
 Qy 98 AspGluLysIleGlnIleValThrGlnMetLeuGluValGluAsnArgAlaArgGln 117
 Db 1102 GATGAGAGATCCAGATCGTGATCAGATGTTGGAGCTGGTGAGAACCGCAGCAGACAG 1161
 Qy 118 MetGluLeuHisSerGlnCysPhe-----GlnAspProAlaGluSerGluArgAla 134
 Db 1162 GTGGACAGTCACGTGGAGCTCTTCAAGCACACACAGGACATCAGTCAGCGCCTGTGTGC 1221
 Qy 135 SerAspLysAlaLysMetAspSerSerGlnProGluArg----- 147
 Db 1222 AGCGCAAGGGCGGCGCAGGACAAGTCGAAGAGTGAAGCCCATCACACAGCAGATAGCCG 1281
 Qy 148 SerSerArgAtqProArgGlnArgThrSerGluSerArgAspLysCysHisMetAla 167
 Db 1282 AATAACACAGCGTCCAGGAGGCGGCAACAAATAGATTCGAGAGAACCGCTCGAATAAT 1341
 Qy 168 AsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLys 187
 Db 1342 CACGACCATGATGACATCACCTCAGGACCGCCCAAGGAGAGAAAGAAACCTCAAAG 1401
 Qy 188 LysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle 207
 Db 1402 AAGAAGAAACCGCTCCAAAGGCCCAAGACAGAGAGGGAAGCGTCTCTCCGCCCATTC 1461
 Qy 208 AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly 227

Db 1462 GACCCCAACAGAGCCACAGTACTCTGTGTCAACAGAGTCTCTTACCGGGAGATGATCGGC 1521
 QY 228 CysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyr 247
 Db 1522 TGTGACACAGCAAGATGCCCATCGAGTGGTTCCTCTCTCCGTGGGGCTCAACCAT 1581
 QY 248 LysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp 267
 Db 1582 AAACCAAGGGCAAGTGTACTCCCAAGTGCCTGGGGAGAGCGAGAACCATGGAC 1641
 QY 268 LysSerThrGluLysThrLysLysAspArg 277
 Db 1642 AAAGCCCTGGAGAGTCCCAAGAAAGAGAGG 1671

RESULT 7

AAA53792

ID AAA53792 standard; cDNA; 911 BP.

XX

AC AAA53792;

XX

DT 19-DEC-2000 (first entry)

XX

DE Human P37ING1 coding sequence.

XX

p53; tumour; cancer; antibody; hybridisation; exon 1b;
 KW ING1; ing1; p37ING1; oncogene; gene therapy; diagnosis;
 KW proliferation disorder; transformation; transformed cell; human; ds.

XX

OS Homo sapiens.

XX

PN WO200046370-A1.

XX

PD 10-AUG-2000.

XX

PF 04-FEB-2000; 2000WO-US02959.

XX

PR 04-FEB-1999; 99US-0118941.

XX

PA (UNII) UNIV ILLINOIS FOUND.

XX

XX Gudkov A, Zeremski M, Gurova KV, Grigorian IA;

PI

XX WPI; 2000-491278/43.

XX

DR P-PSDB; AAY97244.

XX

Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing
 PT and treating cancer, comprises contacting sample with isolated nucleic
 PT acid comprising sequence of exon 1b and detecting hybridized products

XX

PS Disclosure; Page 122-123; 134pp; English.

XX

Mutations in or loss of the p53 gene occur in more than 50% of
 CC human tumours and tumour cell lines, but functional inactivation of
 CC the p53 pathway occurs in a much larger proportion of tumours. In
 CC many cases the mechanism of functional inactivation of the p53 gene
 CC remains unknown but p53 has been found to act in cooperation with
 CC ING1. Functional cooperation between ING1 and p53 suggested that
 CC ING1 encoded a tumour suppressor protein that functioned within the
 CC p53 pathway. This data suggested a possible role for ING1 in head
 CC and neck cancers and chromosomal location of the ING1 placed it
 CC within a region that is frequently rearranged in head and neck
 CC cancers. Large scale analysis of tumours involving ING1 has not
 CC revealed mutations in ING1 nor significant variations in its
 CC expression suggesting that ING1 was not a useful gene to study in
 CC cancer etiology. However, alternative initiation exons of the ing1
 CC gene, each having their own promoter have been discovered.

CC Expression of one promoter (1a) produces a protein identical to
 CC ING1. Expression of a second promoter (1b) produces a protein having
 CC an identical C-terminal fragment to ING1 but an additional 104
 CC N-terminal amino acids. The newly discovered protein has been
 CC designated p37ING1 (Wild type: p37ING1). p37ING1 has the
 CC characteristics of an oncogene. When overexpressed in cells (even

CC those expressing wild type p53) p37ING1 is able to cause
 CC proliferation or transformation of those cells. Thus detecting a
 CC nucleic acid encoding exon 1b of ing1 by hybridisation with an
 CC isolated nucleic acid having the sequence of exon 1b of ing1
 CC or its antisense sequence can identify individuals expressing the
 CC oncogenic form of ing1. Novel peptide sequences taken from the 104
 CC N-terminal peptide of p37ING1 can also be used to raise antibodies
 CC that can also be used in detection methods for the p37ING1 variant.
 CC The polypeptides may be useful in gene therapy for treatment of cell
 CC proliferation disorders, especially cancers and for diagnosing and
 CC studying cancers.

XX SQ Sequence 911 BP; 228 A; 255 C; 305 G; 123 T; 0 other;

Alignment Scores:

Pred. No.:	1-29e-72	Length:	911
Score:	853.50	Matches:	161
Percent Similarity:	75.74%	Conservative:	45
Best Local Similarity:	59.19%	Mismatches:	51
Query Match:	57.63%	Indels:	15
DB:	21	Gaps:	3

US-09-513-365A-1 (1-280) x AAA53792 (1-911)

QY 18 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer 37
 Db 63 GGGGAGCAGCTCCACCTGGTGAAC---TATGTGGAGGACTACTGTGACTCCATCGAGTCC 119
 QY 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
 Db 120 CTGCCTTTCGACTTGCAGAGAAATGTCTCGCTGATCGGGAGATCGACGCGAAATACCA 179
 QY 58 GluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspLeuAsn 77
 Db 180 GAGATCTCGAAGAGCTGACAGGTCTTACGAGCGCTTCAGTCCGAGACAGACGCGGCG 239
 QY 78 GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly 97
 Db 240 CAGAGCGCGGATGCTGCTGTCAGCGCGCGCTGATCCGACGCCAGGAGCTGGC 299
 QY 98 AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
 Db 300 GACGAGAGATCCAGATCGTGCAGCAGATGTTGGAGCTGTGGAGAACCGCGCGCAG 359
 QY 118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
 Db 360 GTGGACAGCCAGCTGGAGCTGTTCGAGCGCGCAGCAGGAGCTGGCGCAGACAGTGGGCA 419
 QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnPro 145
 Db 420 AGCGGCAGTGTGGCGCGCAGCAGGCCAATGGCGGATGCGTAGCGCAGTCTGCACAGCCC 479
 QY 146 GluArgSerSerArgArgProArgGlnArgThrSerGluSerArgAspLeuCysHis 165
 Db 480 -----AACAGCAAGCGCTCACCGCGGCGCAGCAACACGAGAGAACCGTGAGACGCGTCC 533
 QY 166 MetAlaAsnGlyIleGluAspCysAspGlnProProLysGluLysLysSerLysSer 185
 Db 534 AGCAACACGACGACGACGACGCGCGCTCGCGGCACACCAAGGAGAGAGGCAAGAG 593
 QY 186 AlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPhe 205
 Db 594 TCACAGAGAGAGAGCGCTCCAGGCCAAGCGGAGCGGAGAGCGGTCCCTCGCCGACCTC 653
 QY 206 AlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMet 225
 Db 654 CCCATCGACCCCAAGCAACCCACGACTCTGTCTGTGCAACACGAGTCTCTATGGGAGATG 713
 QY 226 IleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeu 245
 Db 714 ATCGGCTGCGACACGACGAGTGCCTCCATCGAGTGGTTCCTTCTCGTGGTGGGCTC 773
 QY 246 ThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThr 265

774 AATCATAAACCCAGGCGAGTGGTACTGTCTCCCAAGTCCGGGGGAGAGAACGAGAAGACC 833

Qy 266 MetAspLysSerThrGluLysThrLysLysAspArg 277
Db 834 ATGGACAAAGCCCTGGAGAAATCCNAAAAAGAGAGG 869

RESULT 8

AAH28478
ID AAH28478 standard; DNA; 1533 BP.

XX AAH28478;

AC 17-SEP-2001 (first entry)

DE Nucleotide sequence of a human cancer associated antigen.

XX Cancer associated antigen; INGI1; tumour suppressor; cancer; vaccine; ss.

XX Homo sapiens.

PH Key Location/Qualifiers
CDS 451..1290

FT FT /tag= a
FT FT /transl_except= "(pos: 817..819, aa: Val)"
FT FT /transl_except= "(pos: 835..837, aa: Val)"
FT FT /transl_except= "(pos: 853..855, aa: Asn)"
FT FT /transl_except= "(pos: 859..861, aa: Asp)"
FT FT /transl_except= "(pos: 865..867, aa: Val)"
FT FT /transl_except= "(pos: 874..876, aa: Ser)"
FT FT /product= "cancer associated antigen"

XX WQ200147959-A2.

XX 05-JUL-2001.

XX 29-NOV-2000; 2000WO-US42334.

XX 30-NOV-1999; 99US-0451739.

XX 24-OCT-2000; 2000US-0602362.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX (CORR) CORNELL RES FOUND INC.

XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;

XX WPI; 2001-441706/47.

XX P-PSDB; AAB84698.

XX Isolated cancer associated nucleic acid molecule identified by SEREX
PT (serological identification of antigens by recombinant expression
PT cloning) technique, useful in nucleic acid based therapies to treat
PT cancer -

XX Claim 1; Page 43-44; 62pp; English.

XX The present sequence encodes a human cancer associated antigen.

CC The sequence is a variant of the INGI1 gene, which is a tumour
CC suppressor gene candidate. The cancer associated antigen polynucleotides
CC and polypeptides are useful for screening for the possible presence of
CC a pathological condition in a subject such as cancer. The cancer
CC associated antigen polypeptides are useful for producing vaccines.

XX Sequence 1533 BP; 336 A; 431 C; 521 G; 244 T; 1 other;

XX Alignment Scores:

Preld. No.: 2,56e-72 Length: 1533
Score: 853.50 Matches: 160
Percent Similarity: 76.30% Conservative: 46
Best Local Similarity: 59.26% Mismatches: 53
Query Match: 57.63% Indels: 11
DB: 22 Gaps: 3

US-09-513-365A-1 (1-280) x AAH28478 (1-1533)

Qy 18 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer 37
Db 469 GGGGAGCAGCTCCACCTGGTGAAC---TATGTGGAGGACTACTCTGGACTCCATCGAGTCC 525

Qy 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
Db 526 CTGCTTTTCGACTTCGACAGAAATGTCTGCTGATGCGGGAGATCGACCGGAATACCAA 585

Qy 58 GluThrLeuLysGluLeuAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77
Db 586 GAGATCCTGAGGAGCTAGACGAGTGTACGAGCGCTTCAGTCGCGAGACAGACGGGGCG 645

Qy 78 GlnLysLysArgLeuGlnGlnLeuLeuArgAlaLeuLeuAsnSerGlnGluLeuGly 97
Db 646 CAGAAAGCGCGATCTGCTGCTGTGTCGCGCGCTGATCCGAGCCAGAGCTGGGC 705

Qy 98 AspGluLysIleGlnIleValThrGlnMetLeuGluValGluAsnArgAlaArgGln 117
Db 706 GACGAGAAGATCCAGATCTGAGCCAGATGTGTGGAGCTGTGTGAGAACCGCAGCGGCGAG 765

Qy 118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArgAlaSerAsp 136
Db 766 GTGGACAGCCAGCTGGAGCTGTTCGAGGCGCAGCAGGAGTGGCGCACACAGCGGCAAC 825

Qy 137 LysAlaLysMetAspSerSerGlnPro-----GluArg 147
Db 826 AGCGCAAGGCTGGCGCGACAGGCCCAAGGCGGCGCAGCGCAGCGCTGACCAAGCCC 885

Qy 148 SerSerArgArgProArgGlnArgThrSerGluSerArgAspLeuCysHisMetAla 167
Db 886 AACACGAAGCGCTCAGCGCGCGCCCAACACGAGAACCGGTGAGAACCGCTCCAGCAAC 945

Qy 168 AsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLys 187
Db 946 CACGACACGACGACGCGCGCTCGGGGCACACCCCAAGGAGAGAGGCGCAAGACCTCCAAG 1005

Qy 188 LysLysLysArgSerLysAlaLysGlnArgGluAlaSerProValGluPheAlaIle 207
Db 1006 AAGAAGAGCGCTCCAAAGCGGAGCGGAGAGCGTCCCTTCGCGCATCCCATC 1065

Qy 208 AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly 227
Db 1066 GACCCCAACGAACCCACCGTACTGTGTGCAACAGGTCTCTATGGGGAGATGATCGGC 1125

Qy 228 CysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyr 247
Db 1126 TCGGACACGACGAGTGGCCCCATCGAGTGTTCACCTTCCTGCTGGGGCTCAATCAT 1185

Qy 248 LysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp 267
Db 1186 AATCCAAAGGCGAAGTGTACTGTCTCCCAAGTCCGGGGGAGACGAGAAGACCATGGAC 1245

Qy 268 LysSerThrGluLysThrLysLysAspArg 277

Db 1246 AAGCCCTGGAGAAATCCAAAAAGAGAGG 1275

RESULT 9

ABK86977

ID ABK86977 standard; cDNA; 2897 BP.

XX ABK86977;

XX 24-SEP-2002 (first entry)

XX Human inhibitor of growth 1 (ING1) isoform, p31ING1b, cDNA.

XX Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1;
KW INGI1; tumour suppressor; cell cycle; breast tumour; lymphoid malignancy;
KW cell growth; anti-ING1; CAB; isoform; diagnosis; tumour; antigen;
KW p31ING1b.

XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 873..1712
 XX FT /*tag= a
 XX FT /product= "p33INGlb"
 XX PN US2002039735-A1.
 XX XX
 XX PD 04-APR-2002.
 XX PF 04-JUN-2001; 2001US-0874347.
 XX PR 02-JUN-2000; 2000US-208829P.
 XX PR 26-FEB-1999; 99US-0258372.
 XX PR 15-NOV-1996; 96US-0751230.
 XX PR 08-DEC-1995; 95US-0569721.
 XX PR 22-MAR-2000; 2000US-0532868.
 XX PA (RIAB//) RIABOWOL K T.
 XX PA (BOLA//) BOLAND D.
 XX PI Riabowol KT, Boland D;
 XX DR WPI; 2002-526652/56.
 XX DR P-PSDB; AAU79587.
 XX XX
 XX PT Novel monoclonal antibody which specifically recognizes epitope of
 XX PT INGI, inhibitor of growth 1 protein, and designated CAB1-10, useful for
 XX PT detecting two different isoforms of INGI and diagnosing a medical
 XX PT condition
 XX PS Disclosure; Page 10-12; 15pp; English.
 XX XX
 CC The invention discloses monoclonal antibodies which can be used, in
 CC combination, to specifically recognise epitopes of INGI (inhibitor of
 CC growth 1) protein isoforms. INGI is a tumour suppressor gene and its
 CC expression is regulated through the cell cycle, peaking in the S phase.
 CC Expression of INGI is down regulated in breast tumours and lymphoid
 CC malignancies. Overexpression of a construct containing the INGI gene is
 CC able to inhibit cell growth by reducing the fraction of cells which enter
 CC into the S phase. The monoclonal antibodies are useful for detecting an
 CC INGI protein in a cell, which involves selecting a cell that ectopically
 CC or endogenously expresses INGI protein. The anti-INGI monoclonal antibody
 CC combination consists of two or more antibodies of CAB1-CAB10 (not
 CC defined), preferably a mixture of CAB1-CAB4, which can detect at least
 CC two different isoforms of INGI. The antibodies are also useful for
 CC diagnosing a disease e.g. tumour or medical condition in an animal
 CC (preferably, human) associated with aberrant levels of an INGI protein.
 CC The sequence presented is the human inhibitor of growth 1 (INGI) isoform,
 CC p33INGlb, cDNA, isolated from a human cDNA library, which encodes a
 CC protein used to raise antibodies.
 XX SQ Sequence 2897 BP; 733 A; 710 C; 819 G; 635 T; 0 other;
 Alignment Scores:
 Pred. No.: 5.89e-72 Length: 2897
 Score: 853.50 Matches: 160
 Percent Similarity: 76.30% Conservative: 46
 Best Local Similarity: 59.26% Mismatches: 53
 Query Match: 57.63% Indels: 11
 DB: 24 Gaps: 3
 US-09-513-365A-1 (1-280) x ABK86977 (1-2897)
 QY 18 GlycyluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer 37
 Db 891 GGGGAGCAGCTCCACCTGGTGAAC---TATGTGAGGAGACTACCTGGACTCCATCGAGTCC 947
 QY 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
 Db 948 CTGCTTTTCGACTTGCAGAGAAATGCTCTGCTGATGCGGGGAGATCGACGCGAATACCAA 1007

QY 58 GluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77
 Db 1008 GAGATCCTGAAGGAGCTAGACGAGTCTACGAGCGCTTACGTGCGGAGACAGACGGCGG 1067
 QY 78 GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly 97
 Db 1068 CAGAGCGGCGGATGCTGCACTGTGTGCGCGCGCTGATCCGCGACCGAGGAGTGGC 1127
 QY 98 AspGluLysIleGlnIleValThrGlnMetLeuLeuValGluAsnArgAlaArgGln 117
 Db 1128 GACGAGAAGATCCAGATCGTGCAGCGAGTGGTGGAGTGGTGGAGAACCGCACCGGCGAG 1187
 QY 118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArgAlaSerAsp 136
 Db 1188 GTGGACAGCCACGTGGAGCTGTCGAGGCGCAGCAGGAGCTGGGCGCACAGCGGCGAAC 1247
 QY 137 LysAlaLysMetAspSerSerGlnPro-----GluArg 147
 Db 1248 AGCGGCAAGGCTGGCGCGGACAGCGCCCAAGCGGAGCGGCGCAGCGAGGCTGACAAGCCC 1307
 QY 148 SerSerArgArgProArgGlnArgThrSerGluSerArgAspLeuCysHisMetAla 167
 Db 1308 AACAGCAAGCGCTCACGCGCGGCGAGCGCAACACGAGAACCGTGAGAACCGCTCCAG 1367
 QY 168 AsnGlyIleGluAspCysAspGlnProProLysGluLysLysSerLysSerAlaLys 187
 Db 1368 CAGCACACAGCAGCGCGCTCGGCGCACACCCAGAGAGAAAGGCGCAAGACTCCAG 1427
 QY 188 LysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle 207
 Db 1428 AAGAAGAAGCGCTCCAAAGCGGAGCGGAGAGCGGCTCCCTGCGGACCTCCCATC 1487
 QY 208 AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly 227
 Db 1488 GACCCCAACGAAACCCACGACTGCTGTGTGCACACAGGTCTCTATGGGAGATGATCGGC 1547
 QY 228 CysAspAsnGluGlnCysProIleGluTyrPheHisPheSerCysValSerLeuThrTyr 247
 Db 1548 TGGCAACAGCAGCAGTGCGCCCATCGAGTGTTCATCTTCGTGCGTGGGCTCAATCAT 1607
 QY 248 LysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp 267
 Db 1608 AAACCCAGCGCAAGTGTACTGTCCAAAGTCCGCGGGGAGAACGAGAAGACCATGGAC 1667
 QY 268 LysSerThrGluLysThrLysLysAspArg 277
 Db 1668 AAGCCCTGGAGAAATCCAAAGAGAGAGG 1697
 RESULT 10
 AAAS3789
 ID AAAS3789 standard; cDNA; 1835 BP.
 XX AC
 XX AAA53789;
 XX 19-DEC-2000 (first entry)
 XX XX
 XX Murine ing1 common exon sequence.
 XX DE
 XX XX
 XX KW p53; tumour; cancer; detection; antibody; hybridisation; exon 1b;
 XX KW INGI; ing1; p33INGI; p37INGI; oncogene; gene therapy; diagnosis;
 XX KW proliferation disorder; transformation; transformed cell; mouse; ds.
 XX XX
 XX OS Mus musculus.
 XX PN WO200046370-A1.
 XX XX
 XX PD 10-AUG-2000.
 XX XX
 XX PF 04-FEB-2000; 2000WO-US02959.
 XX XX
 XX PR 04-FEB-1999; 99US-0118941.
 XX XX

PA (UNII) UNIV ILLINOIS FOUND.
 XX
 PI Gudkov, A., Zerevski M., Gurova KV, Grigorian IA;
 XX
 DR WPI; 2000-491278/43.
 DR
 XX
 PT Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing
 PT and treating cancer, comprises contacting sample with isolated nucleic
 PT acid comprising sequence of exon 1b and detecting hybridized products
 XX
 PS Claim 17; Fig 6; 134pp; English.
 XX
 CC Mutations in or loss of the p53 gene occur in more than 50% of
 CC human tumours and tumour cell lines, but functional inactivation of
 CC the p53 pathway occurs in a much larger proportion of tumours. In
 CC many cases the mechanism of functional inactivation of the p53 gene
 CC remains unknown but p53 has been found to act in cooperation with
 CC ING1. Functional cooperation between ING1 and p53 suggested that
 CC ING1 encoded a tumour suppressor protein that functioned within the
 CC p53 pathway. This data suggested a possible role for ING1 in head
 CC and neck cancers and chromosomal location of the ING1 placed it
 CC within a region that is frequently rearranged in head and neck
 CC cancers. Large scale analysis of tumours involving ING1 has not
 CC revealed mutations in ING1 nor significant variations in its
 CC expression suggesting that ING1 was not a useful gene to study in
 CC cancer etiology. However, alternative initiation exons of the ing1
 CC gene, each having their own promoter have been discovered.
 CC Expression of one promoter (1a) produces a protein identical to
 CC ING1. Expression of a second promoter (1b) produces a protein having
 CC an identical C-terminal fragment to ING1 but an additional 104
 CC N-terminal amino acids. The newly discovered protein has been
 CC designated p37ING1 (wild type: p33ING1). p37ING1 has the
 CC characteristics of an oncogene. When overexpressed in cells (even
 CC those expressing wild type p53) p37ING1 is able to cause
 CC proliferation or transformation of those cells. Thus detecting a
 CC nucleic acid encoding exon 1b of ing1 by hybridisation with an
 CC isolated nucleic acid having the sequence of exon 1b of ing1
 CC or its antisense sequence can identify individuals expressing the
 CC oncogenic form of ing1. Novel peptide sequences taken from the 104
 CC N-terminal peptide of p37ING1 can also be used to raise antibodies
 CC that can also be used in detection methods for the p37ING1 variant.
 CC The polypeptides may be useful in gene therapy for treatment of cell
 CC proliferation disorders, especially cancers and for diagnosing and
 CC studying cancers.
 XX
 SQ Sequence 1835 BP; 541 A; 387 C; 468 G; 439 T; 0 other;
 Alignment Scores:
 Pred. No.: 8,55e-62 Length: 1835
 Score: 745.00 Matches: 140
 Percent Similarity: 76.75% Conservative: 35
 Best Local Similarity: 61.40% Mismatches: 43
 Query Match: 50.30% Indels: 10
 DB: 21 Gaps: 2
 US-09-513-365A-1 (1-280) x AA53789 (1-1835)
 QY 60 LeuLysGluLeuAspValTyrGluLysTyrLysGluAspLeuAsnGlnLys 79
 Db 6 CTGAAGGAGTGTGACGACTACTATGAGAGTTCACACGGGAGACAGCGCAGAGAG 65
 QY 80 LysArgLeuGlnGlnLeuGlnArgAlaLeuLeuAsnSerGlnGluLeuGlyAspGlu 99
 Db 66 CGCCGGGTACTGACCTGCTCCAGAGGGCCCTGATCCGACGAGGAGCTAGCGATGAG 125
 QY 100 LysileGlnLeuValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGlu 119
 Db 126 AAGATCCAGATCTGTGATGAGTGTGAGCTGTGAGAGACCGCGACGACAGCTGGAC 185
 QY 120 LeuHisSerGlnCysPhe-----GlnAspProAlaGluSerGluArgAlaSerAsp 136
 Db 186 AGTCACGTGGAGCTCTTCGAAGCACACCGACATCATGTCACGCGACTGTGTGCGCGGC 245

137 LysAlaLysMetAspSerSerGlnProGluArg-----SerSer 149
 Db 246 AAGGCGGCCAGGACAGTTCGAAGATGAGGCCATCACACGCGACAGATAAGCGAATAAC 305
 QY 150 ArgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaGly 169
 Db 306 AAGCGGTCCAGGAGGCGAGCAAAATGAGATTCGAGAGACGCGTCGAATAATCACGAC 365
 QY 170 IleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLysLys 189
 Db 366 CATGATCATCATCCTCAGGAACGCCAAGGAGAGAAAGCAAAACCTCAAGAGAAG 425
 QY 190 LysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspPro 209
 Db 426 AAACGCTCAAGGCCAAAGCAGAGAGGAGGCTCTCTCGCGACCTTCCATCGACCCC 485
 QY 210 AsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAsp 229
 Db 486 AAGGAGGCCACGCTACTGTCTGTCAACAGGCTCTCTACGGGAGATGATCGCTGTGAC 545
 QY 230 AsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysPro 249
 Db 546 AAGCAGAAATGCCCATCGAGTGGTTCACATCTCTCTCGTGGGCTCAACCATAAACCA 605
 QY 250 LysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSer 269
 Db 606 AAGGCAAGTGTGTACTGCCCCAAGTCCGCTGGGAGAGCGAGAGACCATGACCAAGCC 665
 QY 270 ThrGluLysThrLysLysAspArg 277
 Db 666 CTGGAGAGTCCCAAGAAAGAGAGG 689
 RESULT 11
 AAH28479
 ID AAH28479 standard; DNA; 1143 BP.
 AC AAH28479;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE Nucleotide sequence of a human cancer associated antigen.
 XX
 KW Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.
 XX
 OS Homo sapiens.
 FH
 FT Key Location/Qualifiers
 CDS 16..900
 FT /*tag= a
 FT /transl_except= "(pos: 25..30, aa: Cys)"
 FT /transl_except= "(pos: 124..126, aa: Pro, Ala)"
 FT /product= "cancer associated antigen"
 XX
 PN WO200147959-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 29-NOV-2000; 2000WO-US42334.
 XX
 PR 30-NOV-1999; 99US-0451739.
 PR 24-OCT-2000; 2000US-0602362.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
 XX WPI; 2001-441706/47.
 DR P-PSDB; AAB84697.
 XX
 PT Isolated cancer associated nucleic acid molecule identified by SPREX
 PT (serological identification of antigens by recombinant expression

QY 96 LeuGlyAspGluLeuIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
DB 151 CTGGCGGACGAGAAATCATGATCGTGGAGAGTGGTGGAGTGGTGGAGAACCGCAGC 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
DB 211 CGGAGGTGGACAGCCAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
DB 271 GGCAACAGCGGCAAGGTGGCGGACAGCCCAATGGCGATGGTGGAGCGAGTCTGAC 330
QY 144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
DB 331 AAGCCCC-----AACAGCAAGCGCTCACGGCGGCGAGCAACAGCAAGAACCGTGAGAAC 384
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
DB 395 GCGTCCAGCAACACGACACGACGCGGCGCTCGGGCACACCCAGAGGAGAGAGGCC 444
QY 184 LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
DB 445 AAGACCTCCAGAGAGAGAGCGCTCCAGAGCGGAGCGGAGAGCGGTCCCTGCC 504
QY 204 GluPheAlaIleAspProAsnGluProThrCysLeuCysAsnGlnValSerTyrGly 223
DB 505 GACCTCCCATCGACCCCAACAGCCACGACTACTGTCTGTGCAACAGAGTCTCTATGG 564
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal 243
DB 565 GAGATGATCGGTGGACACAGCAGTGGCCCATCGAGTGGTTCATCTCTCGTGGTG 624
QY 244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspGlu 263
DB 625 GGGCTCAATCATAAACCCCAAGGCGAAGTGTACTGTCTCCCAAGTGGCGGGGAGAACGAG 684
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
DB 685 AAGACCATGGACAAAGCCCTGGAGAAATCCAAAGAGAGAG 726

RESULT 13

AAV62285

ID AAV62285 standard; cDNA; 1902 BP.

XX AC AAV62285;

XX DT 18-JAN-1999 (first entry)

XX DE Partial INGI partial cDNA sequence.

XX KW INGI gene; p33INGI; human; apoptosis; cell death; breast cancer;

XX OS Homo sapiens.

XX FT CDS 109..741

XX FT /*tag= a

XX PN WO984102-A2.

XX PD 08-OCT-1998.

XX PF 26-MAR-1998; 98WO-CA00277.

XX PR 27-MAR-1997; 97US-0828158.

XX PA (UYTE-) UNIV TECHNOLOGIES INT INC.

XX PI Garkavtsev I, Helbing CC, Johnston RN, Riabowol K;

XX PI WPI; 1998-542700/46.

DR P-PSDB; AAW79674.

XX Modulating eukaryotic apoptosis by increasing p33INGI activity -
PT using p33INGI derivatives, to induce apoptosis in cancer cells, and
PT in the investigation of apoptotic pathways

XX Example 2; Fig 2; 66pp; English.

XX This is the nucleotide sequence of a human INGI (inhibitor of
CC growth) partial cDNA clone that codes for a p33INGI polypeptide
CC (see AAW79674), a novel inhibitor of cell growth and a candidate
CC tumour suppressor. INGI is a new gene that is expressed in normal
CC mammary epithelial cells, but which is expressed only at lower
CC levels in several cancerous mammary epithelial cell lines and is
CC not expressed in many primary brain tumours. To isolate INGI, a
CC subtractive hybridisation of breast cancer cell line CDNA was
CC performed with cDNA from normal mammary epithelial cells, and
CC subtracted cDNAs were cloned into retrovirus vector pLNCX.
CC Following passage through a packaging line, normal mouse mammary
CC epithelial cells were infected, and infected cells were injected
CC into nude mice. Putative transforming fragments from tumours were
CC isolated by PCR (see AAV62290-91) and subcloned into INCI. An INGI
CC fragment was obtained and used to screen normal human fibroblast
CC and HeLa cell cDNA libraries. 2 Clones were sequenced to obtain
CC the partial INGI sequence. The complete cDNA sequence (see
CC AAV62292) was obtained by RACE. A claimed method to potentiate
CC apoptosis in a eukaryotic cell involves administering an active
CC p33INGI peptide or an oligonucleotide encoding such as a peptide.
CC A claimed method for inhibiting apoptosis in a eukaryotic cell
CC involves administering an antisense oligonucleotide. Also claimed
CC are a method for determining the apoptotic characteristics of a
CC eukaryotic cell, an assay for determining the level of p33INGI
CC activity in a eukaryotic cell, and an isolated eukaryotic cell
CC substantially free of p33INGI biological activity. The invention
CC discloses INGI derivatives or variants that may be used to induce
CC apoptosis in eukaryotic cancer cells.

XX SQ Sequence 1902 BP; 574 A; 390 C; 462 G; 476 T; 0 other;

Alignment Scores:

Pred. No.: 3.85e-60 Length: 1902
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 19 Gaps: 2

US-09-513-365A-1 (1-280) x AAV62285 (1-1902)

QY 56 TyrGlnGluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspArg 75
DB 31 TGGAAACAGATCTCGAAGGAGCTAGACAGTGTCTACGAGCGCTTCAGTGGCAGACAGAC 90
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu 95
DB 91 GGGGCGCAGAGCGCGGATGCTGCATGTGTGACGCGCGCTGATCCGACGACGAGAG 150
QY 96 LeuGlyAspGluLysLysGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
DB 151 CTGGGCGACGAGAGATCCAGATCGTAGCCAGATGTGTGGAGTGTGTGGAGAACCGCAGC 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
DB 211 CGGCAGTGGAGACGCCAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
DB 271 GGCAACAGCGGCAAGGTGGCGGACAGGCCCAATGGCGATGGTGGAGCGAGTCTGAC 330
QY 144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
DB 331 AAGCCCC-----AACAGCAAGCGCTCACGGCGGCGAGCAACAGCAAGAACCGTGAGAAC 384

QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspGlnProProLysGluLysLysSer 183
 Db 385 GCGTCCAGCAACACGACACGACGCGCGCTCGGGCACACCCCAAGGAGAAAGGCC 444
 QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
 Db 445 AAGACTTCCAAAGAAAGACGCTCCAGGCCCAAGCGGAGGAGGCGTCCCTGCC 504
 QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
 Db 505 GACTCTCCCATGACCCCAACGACCAACGATCTGTGTGCAACACGAGTCTCTATGGG 564
 QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGlnTrpPheHisPheSerCysVal 243
 Db 565 GAGATGATCGCTGCGACACGACGAGTGCCTCCATCGAGTGGTTCCACTTCTCGTGGTG 624
 QY 244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
 Db 625 GGGCTCAATCAATCAACCCAAAGGCAAGTGGTACTGTCCCAAGTCCCGGGGGAGAACGAG 684
 QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
 Db 685 AAGACCATGACCAAGCCCTGGAGAAATCCAAAAGAGAGG 726
 RESULT 14
 AAD46126
 ID AAD46126 standard; cDNA; 1905 BP.
 XX
 AC AAD46126;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Human tumour suppressor protein encoding cDNA.
 XX
 KW Human; tumour suppressor protein; cell proliferative disorder; vaccine;
 KW inflammation; brain cancer; adenocarcinoma; cervix cancer; bone cancer;
 KW apoptosis; leukaemia; lymphoma; melanoma; therapy; chromosome 13; gene;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..160
 FT /*tag= a
 FT CDS 161..1036
 FT /*tag= b
 FT /product= "Human tumour suppressor protein"
 FT 3'UTR 1037..1905
 FT /*tag= c
 XX
 PN WO200268468-A2.
 XX
 XX
 PD 06-SEP-2002.
 XX
 XX
 PF 05-FEB-2002; 2002WO-US03235.
 XX
 XX
 PR 27-FEB-2001; 2001US-0793706.
 XX
 PA (PEKE) PE CORP NY.
 XX
 XX
 PI Gong F, Yan C;
 XX
 DR WPI; 2002-698658/75.
 DR P-FSDB; AAE28633.
 XX
 XX New human tumor suppressor proteins, useful for developing human
 PT therapeutic agents, or preventing or treating inflammation, or
 PT disorders associated with cell proliferation, e.g. bone cancer, brain
 PT cancer, leukemia or lymphoma
 XX
 XX Claim 4; Fig 1; 200pp; English.
 PS
 XX The invention relates to human tumour suppressor polypeptides and

CC polynucleotides. Sequences of the invention are useful for diagnosing,
 CC preventing or treating inflammation, or disorders associated with cell
 CC proliferation and apoptosis e.g. bone cancer, brain cancer, cervix
 CC cancer, adenocarcinoma, leukaemia, lymphoma or melanoma. They are
 CC particularly useful as models for developing human therapeutic targets,
 CC identifying therapeutic proteins, or serving as targets for the
 CC development of human therapeutic agents that modulate tumour suppressor
 CC protein activity in cells and tissues that express the tumour suppressor
 CC protein. Polypeptides of the invention are used for identifying agents
 CC that modulate their activity. They are useful for raising antibodies or
 CC eliciting an immune response; as a reagent in assays designed to
 CC quantitatively determine levels of the protein (or its binding partner
 CC or ligand) in biological fluids; or as markers for tissues in which the
 CC corresponding protein is preferentially expressed. The invention is also
 CC used as vaccines. The present sequence is human tumour suppressor
 CC protein encoding cDNA. The tumour suppressor gene is located on
 CC chromosome 13.
 XX

SQ Sequence 1905 BP; 532 A; 428 C; 528 G; 417 T; 0 other;

Alignment Scores:

Pred. No.: 3,868-60 Length: 1905
 Score: 728.00 Matches: 136
 Percent Similarity: 75.22% Conservative: 37
 Best Local Similarity: 59.13% Mismatches: 47
 Query Match: 49.16% Indels: 10
 DB: 24 Gaps: 2

US-09-513-365A-1 (1-280) x AAD46126 (1-1905)

QY 58 GluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspLeuAsn 77
 Db 332 GAGATCTTGAAGGAGCTAGACGAGTGTACGAGCGCTTCAGTCGCAGACAGCGGGCG 391
 QY 78 GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGluLeuGly 97
 Db 392 CAGAAGCGCGGATGTCACCTGTGTGACGCGCGCTGATCCGACGAGGAGCTGGGC 451
 QY 98 AspGluLysIleGlnIleValThrGlnMetLeuGluValGluAsnArgAlaArgGln 117
 Db 452 GACGAGAAGATCCAGATCGTGAGCCAGATGGTGAGAGTGGTGAGAACCGCGACGCGCGAG 511
 QY 118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArgAlaSerAsp 136
 Db 512 GTGGACAGCCACGTGGAGCTGTTGAGGCGCGACGAGAGCTGGCGGCACAGCGGCAAC 571
 QY 137 LysAlaLysMetAspSerSerGlnPro-----GluArg 147
 Db 572 AGCGGCAAGGCTGGCGCGGACAGGCGCCAAAGCGGAGCGGCGAGCGGTGACAAAGCCC 631
 QY 148 SerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAla 167
 Db 632 AACAGCAGCGCTCACGGCGGCGAGCGCAACACAGAGAACCGGTGAGAACCGCGTCCACCAAC 691
 QY 168 AsnGlyIleGluAspCysAspGlnProProLysGluLysLysSerLysSerAlaLys 187
 Db 692 CAGGACACGACGAGCGCGCTCGGGCACACCCAGGAGAGAGAGGCGCAAGCTCCAAG 751
 QY 188 LysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle 207
 Db 752 AAGAAGAGCGCTCCAAGGCCAAGCGGAGCGAGAGGCGTCCCTGCGCACCTCCCATC 811
 QY 208 AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly 227
 Db 812 GACCCCAACGAACCCACGCTACTGTGTGTCACACCGAGGTCTCTATGGGAGAGTATCGGC 871
 QY 228 CysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyr 247
 Db 872 TCGGACACGACGAGTGGTCCCATCGAGTGGTTCCTCTCTCGTGGCGGTCTCAATCAT 931
 QY 248 LysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp 267
 Db 932 AAACCAAGGGCAAGTGGTACTGTCTCCCAAGTCCCGGGGGAGAGACGAGAAGACCATGGAC 991

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2004, 19:38:43 ; Search time 2031 Seconds
(without alignments)
3350.691 Million cell updates/sec

Title: US-09-513-365A-1
Perfect score: 1481
Sequence: 1 MLGQQQQQLYSSAALLTGER.....DNEKTMDSKTEKKDRSR 280

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DRV=xlp
-Q=/cgr2_1/USPTO.spool_p/US09513365/runat_12012004_163932_28778/app_query.fasta_1.455
-DB=EST -Qfmt=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09513365 @CGN 1 1 3549 @runat_12012004_163932_28778 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
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7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1433.5	96.8	2643	11	AK048800	AK048800 Mus muscu
2	1433.5	96.8	2812	11	AK083144	AK083144 Mus muscu
3	1395.5	94.2	1464	11	AK012716	AK012716 Mus muscu
4	1296	87.5	912	13	BQ277444	BQ277444 AGENCOURT
5	1123	75.8	736	13	BQ225297	BQ225297 603799281
6	1121	75.7	892	13	BQ332089	BQ332089 603869689
7	1096.5	74.0	919	10	BG211544	BG211544 RST31111
8	1094	73.9	793	10	BE796780	BE796780 601587557
9	1063	71.8	778	12	BI548536	BI548536 603191255
10	1043	70.4	779	13	BU259874	BU259874 603504254
11	1027	69.3	673	13	BU386788	BU386788 603581891
12	1024	69.1	735	12	BM982877	BM982877 UI-CF-EMI
13	1022	69.0	707	13	BU323498	BU323498 603489003
14	1007.5	68.0	864	13	BU591073	BU591073 AGENCOURT
15	1006.5	68.0	798	10	BG184056	BG184056 RST2972 A
16	965	65.2	927	14	CA973890	CA973890 AGENCOURT
17	961	64.9	664	12	BM713460	BM713460 UI-E-EJ1-
18	950	64.1	728	13	BU613909	BU613909 UI-M-FRO-
19	935	63.1	708	12	BI460319	BI460319 603201967
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22	914	61.7	671	13	BU404104	BU404104 604138228
23	911.5	61.5	859	13	BU000292	BU000292 AGENCOURT
24	902	60.9	891	12	BI091047	BI091047 602855235
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26	889	60.0	679	9	AV647917	AV647917 AV647917
27	883	59.6	564	10	BE839427	BE839427 RC3-PN014
28	874	59.0	538	10	BF523624	BF523624 UI-R-Cl-1
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30	858	57.9	671	9	AL857736	AL857736 AL857736
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
AK048800
Mus musculus 2643 bp mRNA linear HTC 05-DEC-2002
Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:C230071A14 product:inhibitor of growth
family, member 1-like, full insert sequence.
ACCESSION
AK048800
VERSION
AK048800.1 GI:26339579
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Muridae; Sciurognathi; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999) **MB**
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20493374
 PUBMED 11042159

REFERENCE

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Fleischmann, W., Gaasterland, T., Giusti, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,
 Quackenbush, J., Schriml, L. M., Stauble, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K. F., Suzuki, H.,
 Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
 and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851

REFERENCE

5 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 MEDLINE 12600000
 PUBMED 12026433

REFERENCE

6 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yaeunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome

REFERENCE

7 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome

COMMENT

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/.

FEATURES

Location/Qualifiers

source

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 /clone="C230071A14"
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 /note="unnamed protein product: inhibitor of growth
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 evidence: BLASTN, 98%, match=971)
 putative"

CDS

683 a 557 c 710 g 693 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,33e-82 Length: 2643
 Score: 1433.50 Matches: 271
 Percent Similarity: 98.58% Conservative: 6
 Best Local Similarity: 96.44% Mismatches: 3
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US-09-513-365A-1 (1-280) x AK048800 (1-2643)

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 QY 40 HisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThr 59
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QY 240 PheSerCysValSerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArg 259

Db 1196 TTTTCATGTGTTTCATCTACCTATAACCCAGGAGGATGTTGTTGCCAAAGTGTAGG 1255

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QY 280 Arg 280

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RESULT 2

AK083144

LOCUS

DEFINITION Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone: C630016P10 product: inhibitor of growth family, member 1-like, full insert sequence.

ACCESSION AK083144

VERSION 1

KEYWORDS HTC; CAP trapper.

SOURCE 1 GI:26350286

ORGANISM Mus musculus (house mouse)

REFERENCE 1 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, H., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Washiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Giusti, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Wagner, K., Washio, T., Sakai, K., Okido, F., Furuno, M., Aono, H., Balardini, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 6

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

PLEASE VISIT OUR WEB SITE FOR FURTHER DETAILS.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

FEATURES

source

1. .2812

Location/Qualifiers

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CDS

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QIVTQMLEVNRAROMELHSOCFOPAESRASDKSKMDSOPERSRPRPRORTSE
SDLCHMTNGIDDCDDPPKRSKSKAKKRSKAKQEREASPFVPAIDPNPTVCLC
NOVSGEMIGCDNEQCPIEWFSCVSLTYKPKRWIKPCRCRGNDEKTKMSTKTKK
ERROR"

BASE COUNT 725 a 589 c 743 g 753 t 2 others
ORIGIN

Alignment Scores:

Pred. No.: 1.39e-82 Length: 2812
Score: 1433.50 Matches: 271
Percent Similarity: 98.58% Conservative: 6
Best Local Similarity: 96.44% Mismatches: 3
Query Match: 96.79% Indels: 1
DB: 11 Gaps: 1

US-09-513-365A-1 (1-280) x AK083144 (1-2812)

QY 1 MetLeuGly---GlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGlu 19
DB 479 ATGTTAGGAGCAGCAGCAGCAGCAGCTGTACTCTGCGCCCGCTCTCTGACCGGAGAG 538
QY 20 ArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuPro 39
DB 539 CGGAGCGCGTCT 598
QY 40 HisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThr 59
DB 599 CACGACATGACAGAGAACGTGCTCGTCTGCGGAGCTGGACAAACAAATACCAAGAACG 658
QY 60 LeuLysGluLeuLeuAspValTyrGluLysTyrLysLysLysLysLysLysLysLys 79
DB 659 TTAAGGAATTCATGCTATGCTATGAAATAATTAAGAAAGATGATTCACACACAGAAA 718
QY 80 LysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGlnLeuGlyAspGlu 99
DB 719 AAACGCTACAGCAGCATCTCCAGAGAGCGTTAATCAATAGCCCAAGATTTGGGAGATGAA 778
QY 100 LysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGlu 119
DB 779 AAAATTCAGATTCTCACCCAGATGCTCGAATTTGGTGGAGAACCGAGCAGACAAATGGAG 838
QY 120 LeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLys 139
DB 839 CTCATTTCAGTGTTTCAGAGATCTCTCTGAAAGTGAGCGAGCCTCAGACAAAGTGAAG 898
QY 140 MetAspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGlu 159
DB 899 ATGGATTCCAGTCAACCGGAAGATCTCTAGAGACCTCGAGAGACGAGGACCACTGAG 958
QY 160 SerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLys 179
DB 959 AGCCGTGACTTATGTACATGACAAACCGGATTTGACGACTGTGATCATCAACCCAGAAA 1018
QY 180 GluLysLysSerLysSerAlaLysLysLysLysLysLysLysLysLysLysLysLys 199
DB 1019 GAAAGAGATCCCAAGTCCCGCAAGAGAGAACGCTCCCAAGGCCCAAGCAGGAGGGAG 1078
QY 200 AlaSerProValGluPheAlaLysAspProAsnGluProThrTyrCysLeuCysAsnGln 219
DB 1079 GCATCCCTGTCAGTTTGCCATCGATCCCAATGAGCCCACTTACTTCTGTGTACCAA 1138

QY 220 ValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTyrPheHis 239
DB 1139 GTGCTCTACGGGAGATGATAGCTGTGACATGACAGTGTCCCATGTAATGTTTCAC 1198
QY 240 PheSerCysValSerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArg 259
DB 1199 TTTTCATGTGTTTCACTCACTTATTAACCCAGGGGAAATGATTTGCCAAAGTGTAGG 1258
QY 260 GlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSer 279
DB 1259 CGAGCAATGAGAAAACCATGACAAAAGTACCGAAAACAAAAAGAGAGAGAGCG 1318
QY 280 ATG 280
DB 1319 AGG 1321
RESULT 3
AK012716 1464 bp mRNA linear HTC 05-DEC-2002
LOCUS Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DEFINITION enriched library, clone:281001M06 product:inhibitor of growth
family, member 1-like, full insert sequence.
ACCESSION AK012716
VERSION AK012716.1 GI:12849649
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nukado, I., Pesole, C.,
Quackenbush, J., Schriml, L. M., Staib, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bul, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,

RESULT 4
 BQ277444
 LOCUS
 DEFINITION BQ277444 912 bp mRNA linear EST 07-MAY-2002
 AGENCOURT_6738254 NIH_MGC_127 Homo sapiens cDNA clone IMAGE:5810745
 5', mRNA sequence.
 ACCESSION BQ277444
 VERSION
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 912)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: NCI
 CDNA Library Preparation: Michael Brownstein Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM2058 row: h column: 10
 High quality sequence stop: 587.
 Location/Qualifiers

FEATURES
source

1..912
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5810745"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="PH10B (T1-phage-resistant)"
 /clone_lib="NIH MGC 127"
 /notes="Vector: pDNR-LIB; Site 1: Sfil (ggccattatggcc);
 Site 2: Sfil (ggccctcgcc); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
 ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
 gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
 used in cloning as follows:
 5'-AACGATGGTATCAGCGAGTGGCCATTACGGCGGG-3' and
 5'-ATTCTAGAGCCGAGCGCGGCATG-3'. Full-length
 enriched library was constructed using the Clontech
 Creator SMART kit and size-selected to contain the 1-2 kb
 size fraction (other fractions present in NIH MGC 126 and
 NIH MGC 128). Library created in the laboratory of T.
 Udén, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC
 Library."

BASE COUNT 313 a 184 c 235 g 180 t

ORIGIN

Alignment Scores:
 Pred. No.: 4,04e-74 Length: 912
 Score: 1296.00 Matches: 261
 Percent Similarity: 92.71% Conservative: 6
 Best Local Similarity: 90.62% Mismatches: 11
 Query Match: 87.51% Indels: 11
 DB: 13 Gaps: 1

US-09-513-365A-1 (1-280) x BQ277444 (1-912)

QY 1 MetLeuGlnGlnGlnGlnGlnLeuTySerSerAlaAlaLeuLeuThrGlyGluArg 20
 Db 22 AUGTTAGGCGAGCAGCAGCAGCAGCACTGACTCGCTCGCTCGCTCTCTGACCGGGAGCGG 81
 QY 21 SerArgLeuLeuThrCysTyValGlnAspTyLeuGluCysValGluSerLeuProHis 40
 Db 82 AGCGGCTGCTCACCTGTACGTGACGTGACAGGACTACCTTGAGTGGCTGGAGTCGCTGCCAC 141

QY 41 ApMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyTrGlnGluThrLeu 60
 Db 142 GACATGCAGAGGAAGCTGTCTGTGTCGAGAGCTGGACACAATATATCAAGAAAGTTA 201
 QY 61 LysGluIleAspAspValTyTrGluLysTyTrLysLysGluAspAspLeuAsnGlnLysLys 80
 Db 202 AAGGAAATTGATGATGTCTACGAAATATATAGAAAGAAGATGATTTAAACCCAGAAGAA 261
 QY 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100
 Db 262 CGTCTACAGCAGCTTCTCCAGAGACCTAATTAATAGTCAAGAATTGGGAGATGAAAAA 321
 QY 101 IleGlnIleValThrGlnMetLeuGluValGluAsnArgAlaArgGlnMetGluLeu 120
 Db 322 ATACAGATTGTACACAATGCTCGAATGTGGTGGAAATCGGCAAGACAAATGGAGTTA 381
 QY 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
 Db 382 CACTCACAGTGTTCCTCAAGATCCTCTGAAAGTGAACGAGCCTCAGATAAAGCAAGATG 441
 QY 141 ApSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 160
 Db 442 GATTCAGCAGCAACCAAGAGATCTTCAAGAGACCCCGCAGCAGCGGACCGTGAAGC 501
 QY 161 ArgAspLeuCysHisMetAlaAsnGlyTleGluAspCysAspAspGlnProProLysGlu 180
 Db 502 CGTGATTTATGTGCATGCGCAATGGGATTGAAGACTGTGATGATCAGCCACCTAAGAA 561
 QY 181 LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla 200
 Db 562 AAGAAATCCAGTCAGCAAGAAAAAGAAACGCTCCAGGGCAAGCAGGAAAGGGAAGCT 621
 QY 201 SerProValGluPheAlaIleAspProAsnGluProThrTyTrCysLeuCysAsnGlnVal 220
 Db 622 TCACCTGTGTAGTTTGCAATAGATCCTAATGAACCTACATACCTGTTATGCAACCCAGTG 681
 QY 221 SerTyGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluThrPheHis-Ph 240
 Db 682 TCTTATGGGAGATGATGAGTGTGCAATGA- CAGTGTCCAATGGAATGGGTTCACCTTT 740
 QY 240 eSerCysValSerLeuThrTyTrLys- ProLysGlyLysTyTrTyTr- CysProLysCysArg 259
 Db 741 TTCATGTGTTTCACTTACCTATAAACCCCAAGGGGAAATGGTATTGTCACCAAGTCAGG 800
 QY 260 -GlyAspAsn-----GluLysThrMetAspLysSerThrGluLysTh 273
 Db 801 GGGAGATAATGGAGAAAAAACCATGGGACAAAAAAGTACCTGGAAAAAGGACCAAAAAAGAA 860
 QY 273 LysLysAspArgArg 278
 Db 861 TAGAAAAGATCCAAAG 876

RESULT 5
 BQ225297
 LOCUS
 DEFINITION BQ225297 736 bp mRNA linear EST 26-NOV-2002
 603799281F1 CSEQCHN23 Gallus gallus cDNA clone ChEST768a21 5', mRNA
 sequence.
 ACCESSION BQ225297
 VERSION BQ225297.1 GI:25461055
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 736)
 AUTHORS Boardman, P. E., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,
 Pong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392

COMMENT

Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1. 736
 Location/Qualifiers
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CHEST768a21"
 /dev_stage="22"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN23"
 /note="Organ: heads; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT 242 a 163 c 191 g 140 t

ORIGIN

Alignment Scores:

Pred. No.: 4,396-63 Length: 736
 Score: 1123.00 Matches: 208
 Percent Similarity: 92.98% Conservative: 17
 Best Local Similarity: 85.95% Mismatches: 17
 Query Match: 75.83% Indels: 0
 DB: 13 Gaps: 0

US-09-513-365A-1 (1-280) x BU225297 (1-736)

QY 39 ProHisaspMetGlnArgasnValSerValLeuArgGluLeuAspAsnLysTyrGlnGlu 58
 DB 3 CCCTGAAGGAATACAGCGCTCTATGAAAATACAGTCTGAGAACGATCCGTCAG 62
 QY 59 ThrLeuLysGluLeuAspValTyrGluLysTyrLysGluAspAspLeuAsnGln 78
 DB 63 GCTTTAAGGAATACAGCGCTCTATGAAAATACAGTCTGAGAACGATCCGTCAG 122
 QY 79 LysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGluLeuGlyAsp 98
 DB 123 AAGAAACGCTTGCCAGCAGCAGCTCCAGCGGCTTTAATCAACAGTCAAGAACGAT 182
 QY 99 GluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMet 118
 DB 183 GAGAAATTCAGATAGTACTGAGTCTGGAATCTGTAGAGAAATAGAGCCGACAGATG 242
 QY 119 GluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAla 138
 DB 243 GAACACACTCTCAGTGTCTTTCAGGATCTGCTGAAAACGACAAAGCCTCGGAAAGGCC 302
 QY 139 LysMetAspSerSerGlnProGluArgSerSerArgProArgArgGlnArgThrSer 158
 DB 303 AAGATGGAGTCTGCGCAGCCAGAGATCATCTACTAGACCTCGTCTGCGCAGGAAACGAGC 362
 QY 159 GluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProPro 178
 DB 363 GAGAGCGCGACCTGTGGCATATAGCACCGGATCGATGACTGCGACGATCAGCCACCT 422

QY 179 LysGluLysLysSerLysSerLysLysLysLysLysLysLysLysLysLysLysLysLys 198
 DB 423 AAAGAGAAAAGATCGAAATCTTCCAAAGAAAACGCTCCAAAGCCAAACAGAGAGG 482
 QY 199 GluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsn 218
 DB 483 GAGGTTTCCACCGTGGAGTTTGGATTTGATCCCAATGAACCGGACTTACTGCTTATGTAAC 542
 QY 219 GlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTyrPhe 238
 DB 543 CAAAGTGTCTTACGGCGAATGATAGGTGTGATACGACAGTGTCTTATGAGTGGTTC 602
 QY 239 HisPheSerCysValSerLeuThrTyrLysProLysGlyLysLysTyrCysProLysCys 258
 DB 603 CACTTCTCGTGTGGACTCACCTATAAACCCGAGGGGAAATGGTATTGCCCAAGTGC 662
 QY 259 ArgGlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArg 278
 DB 663 AGAGGAGATACGAGAAAACGATGGACAAATGTACTGACAAATCAAAAAAGGATAGAAGA 722
 QY 279 SerArg 280
 DB 723 TCGAGG 728
 RESULT 6
 LOCUS BU332089 892 bp mRNA linear EST 28-NOV-2002
 DEFINITION 603869689F1 CSEQCHN65 Gallus gallus cDNA clone CHEST894a23 5', mRNA sequence.
 ACCESSION BU332089
 VERSION BU332089.1 GI:25840090
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 12445392
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1. 892
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CHEST894a23"
 /tissue_type="whole embryo"
 /dev_stage="10"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN65"
 /note="Organ: whole embryo; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2

FEATURES

source

rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT 284 a 190 c 224 g 194 t
ORIGIN

Alignment Scores:

Pred. No.: 6.8e-63 Length: 892
Score: 1121.00 Matches: 210
Percent Similarity: 93.06% Conservative: 18
Best Local Similarity: 85.71% Mismatches: 16
Query Match: 75.69% Indels: 1
DB: 13 Gaps: 0

US-09-513-365A-1 (1-280) x BU332089 (1-892)

QY 37 SerLeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAenLysTyr 56
DB 12 TCCTGCGCTGACATCCAGCCACGTCGCTGCTGCGGAGGTGGACACCCGGTGC 71.
QY 57 GlnGluThrLeuLysGluLeuAspValTyrGluLysTyrLysLysGluAspLeu 76
DB 72 CAAGAAGCTTTAAAGCAATAGACGCTCTATGAAAAATACAAAGTCTGAGAAGCATCT 131
QY 77 AsnGlnLysLysArgGlnGlnLeuLeuGlnArgAlaLeuLeuLeuSerGlnGluLeu 96
DB 132 GCTCAGAAGAAACGCTTGCAGCAGCACCTCCAGCGGCTTTATCAACAGTCAAGAACATC 191
QY 97 GlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArg 116
DB 192 GGAGATGAGAAATTCAGATGTTACTCAGATCTGGAATGCTGATAGATAGAGCCCA 251
QY 117 GlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAsp 136
DB 252 CAGATGGAAACACACTCTCAGTCTGTTTTCAGGATCTGCTGAAACGACCAAGCTCTGGAA 311
QY 137 LysAlaLysMetAspSerSerGlnProGluArgSerArgArgProArgGlnArg 156
DB 312 AAGCCCAAGATGAGGTCCTGCCAGCCAGAGATCATCAGTAGACCTCGTCGGCAGCGA 371
QY 157 ThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGln 176
DB 372 ACCAGCGAGAGCGCCGACCTGTCCTATAGCCACCGGATCGATGACTGCGACGATCAG 431
QY 177 ProProGluLysLysSerLysSerAlaLysLysLysArgSerLysAlaLysGln 196
DB 432 CCACCTTAAGAGAAAGATCGAAATCTTCCAGAGAAACCGCTCCAAAGCCAAACAA 491
QY 197 GluArgGluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeu 216
DB 492 GAGAGGGAGGTTTCCACCGGGAGTTTGGCATTTGATCCCAATGAACCGACTTACTGCTTA 551
QY 217 CysAsnGlnValSerTyrGlyGluMetIleGlyCysAsp-AsnGluGlnCysProIleG1 236
DB 552 TGTAACCAAGTGCTTACGGCGAAATGATAGGATGTGATTAACCAACAGTGCTTATGA 611
QY 236 uTPpHeHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysPr 256
DB 612 GTGTTCCACTTCTCGTGTGTGGACTCACCTATAAACCGAGGGGAAATGGTATTGCC 671
QY 256 oLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAs 276
DB 672 CAATGTCAGAGAGATAACGAGAAACGATGGTGAATAATGTACTGACAAATCAAAACAGGA 731
QY 276 pArgArgSerArg 280
DB 732 TAGAAGATCGAGG 744

RESULT 7

LOCUS BG211544

DEFINITION RST31111 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
EST 21-APR-2001

ACCESSION BG211544
VERSION BG211544.1 GI:13733231
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 919)

Harrington,J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,

Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,

Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith

, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher

, J., Danzig, J., and Ducar, M.

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

21227151

11329013

COMMENT

Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@athersys.com

High quality sequence stop: 439.

Location/Qualifiers

1..919

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/cell_line="HT1080"

/clone_lib="Athersys RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression

Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the

cell type indicated is HT1080, since a random activation

method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."

332 a 151 c 216 g 216 t 4 others

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 2.6e-61 Length: 919
Score: 1096.50 Matches: 214
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 95.11% Mismatches: 7
Query Match: 74.04% Indels: 4
DB: 10 Gaps: 1

US-09-513-365A-1 (1-280) x BG211544 (1-919)

QY 58 GluThrLeuLysGluLeuAspValTyrGluLysTyrLysLysGluAspLeuAsn 77
DB 4 GAAAGCTTAAAGAAATTCATGATGCTACGAAAAATATAAGAAAGAGATGATTTAAAC 63
QY 78 GlnLysLysArgLeuGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGluLeuGly 97
DB 64 CAGAAGAAACGCTCAGCAGCTTCTCCAGAGACACTAATTAATAGTCAAGATTTGGGA 123
QY 98 AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
DB 124 GATGAAAAATACAGATTTTACACAAATGCTCGAATTCGTGGAATTCGGCAACACAA 183
QY 118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLys 137
DB 184 ATGGAGTTACACTCAGCTGTTTCCAGATCTCTGCTGAAAGTCAACAGCCTCAGATAA 243
QY 138 AlaLysMetAspSerSerGlnProGluArgSerArgArgProArgGlnArgThr 157
DB 244 GCAAGATGATGATTCAGCCCAACAGAAAGATCTTCAAGAAAGACCCCGCAGGCGGACC 303
QY 158 SerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnPro 177

JOURNAL
COMMENT

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11661 row: n column: 13
High quality sequence stop: 775.

FEATURES

source

1..778
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5262540"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: Sali-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTTWN-3', size-selected for average insert size 2.5 kb and normalized to 10⁷. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
237 a 176 c 227 g 138 t

BASE COUNT
ORIGIN

Alignment Scores:

Pred. No.: 3,256-59 Length: 778
Score: 1063.00 Matches: 215
Percent Similarity: 98.63% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 71.78% Indels: 2
DB: 12 Gaps: 0

US-09-513-365A-1 (1-280) x B1548536 (1-778)

QY 1 MetLeuGlyClnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg 20
DB 124 ATGTTAGGCGAGCAGCAGCAACTGTACTCGTGGCTGCGCTCTCGACCGGGAGCG 183
QY 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40
DB 184 AGCCGCTGCTCACCTGCTACGTGCGAGGACTACCTTGAGTGGTGCGTGCACAC 243
QY 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
DB 244 GACATGCAGGAGCACTGTCTGCTGCGAGAGCTGGACACAAATATCAAGAAAGTTA 303
QY 61 LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
DB 304 AAGGAAATTCATCATCTCTACGAAATAATAAGAAAGAGATGATTTAAACCAAGAGAAA 363
QY 81 ArgLeuGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100
DB 364 CGTCTACAGAGCTTCTCAGAGAGCACTAATTAATAGTCAAGAAATGGAGATGAAAA 423
QY 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120
DB 424 ATACAGATTGTTACAAATGCTCGAATTTGTTGAAATCGGCAAGACAAATGGAGTTA 483
QY 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
DB 484 CACTCACAGTGTTCAGATCTCTGTAAGTGAACGAGCCTCAGATAAGCAAGATG 543
QY 141 AspSerSerGlnProGluArgSerSerArgArgProArgProArgGlnArgThrSerGluSer 160

DB 544 GATTCACGCCAACCAAGATCTTCAAGAACCCCGCAGCGAGCCAGTGAAGC 603
QY 161 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProLysGlu 180
DB 604 COTGATTATGTACATGCAATGGATTGAAGACTGTGATGATGATGATGATGATGAT 663
QY 181 LysLysSerLysSerAlaLysLysLysLysLysLysLysLysLysLysLysLysLys 200
DB 664 AAGAATTCAGTTCAGCAAGAAACGCTCAAGGC-AAGCAGGAAGAGGAGT 722
QY 201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysGln 219
DB 723 TCACCTGTTGAGTTTC-ATAGATCTTAATGAACCTACATACCTGTTATGCAACAG 778

RESULT 10

BU259874

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

779 bp mRNA linear EST 26-NOV-2002
603504254F1 CSEQCHN51 Gallus gallus cDNA clone CHEST426k14 5', mRNA
sequence.

BU259874

BU259874

EST.

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 779)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

22335534

12445392

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Location/Qualifiers

1..779

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, Hisex"

/db_xref="taxon:9031"

/clone="CHEST426k14"

/dev_stage="22"

/lab_host="DH10B"

/clone_lib="CSEQCHN51"

/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:

ECORI; Site_2: NotI; This normalized library was

constructed from 1 million independent clones. cDNA

synthesis was initiated using an oligo(dT) primer, using

methylated C in the first strand synthesis reaction.

Following this first strand reaction, double-stranded cDNA

was blunted, ligated to NotI adapters, digested with EcoRI

size-selected, and cloned into the NotI and EcoRI

compatible sites of a custom modified MCS of the

pBluescript (KS+) vector. The library was normalized in 2

rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6

(1996): 791, except that a significantly longer

reannealing hybridization was used."

261 a 155 c 191 g 171 t 1 others

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 6,256-58 Length: 779

Score: 1043.00 Matches: 193

Percent Similarity: 94.06% Conservative: 13
 Best Local Similarity: 88.13% Mismatches: 13
 Query Match: 70.43% Indels: 0
 DB: 13 Gaps: 0

US-09-513-365A-1 (1-280) x BU259874 (1-779)

QY 62 GluLeuAspValTyrGluLysTyrLysLysGluAspLeuAenGlnLysLysArg 81
 Db 2 GAAATAGACGACGCTATGAAATAAATCAAGCTGTGAGAACGATCTGCTCAGAGAAACGC 61

QY 82 LeuGlnGlnLeuGlnArgAlaLeuLeuAenSerGlnGlnLeuGlnLysLysIle 101
 Db 62 TTCAGCAGCACCTCCAGCGGGCTTTAATCAACAGTCAAGAACTCGGAGATGAGAAAT 121

QY 102 GlnIleValThrGlnMetLeuGluLeuValGluAenArgAlaArgGlnMetGlnLeuHis 121
 Db 122 CAGATAGTACTCAGATGCTGGAACTGTGAGAAATAGACCCACAGATGGAACACAC 181

QY 122 SerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMetAsp 141
 Db 182 TCTCAGTGTCTTTCAGGATCTGTGAAACGACCAAGCTCTGGAAGGCGCAAGATGGAG 241

QY 142 SerSerGlnProGluArgSerArgArgProArgArgGlnArgThrSerGluSerArg 161
 Db 242 TCTGCGCAGCCAGAGATCATCAGCTAGACCTCTGCGCAGCGAAACAGCGAGAGCCGC 301

QY 162 AspLeuCysHisMetAlaAenGlyIleGluAspCysAspAenGlnProProLysGluLys 181
 Db 302 GACCTGTGCATATAGCAACGGGATCGATGATGCGACGATCAGCCACCTAAAGAGAAA 361

QY 182 LysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSer 201
 Db 362 AGATCGAATCTTCCAGAGAAACAAACGCTCCAAAGCCAAACAGAGAGGGAGTTTCA 421

QY 202 ProValGluPheAlaLeuAspProAenGluProThrTyrCysLeuCysAenGlnValSer 221
 Db 422 CCGCTGGAGTTTGGATGTATGCTCAATGAAACCGACTTACTGCTTATGTAACCAAGTGTCT 481

QY 222 TyrGlyGluMetIleGlyCysAspAenGluGlnCysProIleGluThrPheHisPheSer 241
 Db 482 TAGCGGGAATGATAGATGTGATAACGAACATGCTCTATTGAGTGGTTTCCACTTCTCG 541

QY 242 CysValSerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAsp 261
 Db 542 TGTGTGGACTACCTATATAACCGAAGGGAATGTTATGGCCCAAGTGCAGAGAGAT 601

QY 262 AsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg 280
 Db 602 AACGAGAAACGATGACAAATGTACTGACAAATCAAAAAGGATAGAGATCGAGG 658

RESULT 11
 BU386788 673 bp mRNA linear EST 28-NOV-2002
 LOCUS 603581891F1 CSFQCHN75 Gallus gallus cDNA clone CHEST531f23 5', mRNA
 DEFINITION sequence.
 ACCESSION BU386788
 VERSION BU386788.1 GI:25894789
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 673)
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences

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 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk

Location/Qualifiers
 1. 673
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CHEST531f23"
 /dev_stage="36"
 /lab_host="DH10B"
 /clone_lib="CSFQCHN75"
 /note="Organ: trunks; Vector: pBluescript II KS(+);
 Site_1: EcoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunted, ligated to NotI adapters, digested with EcoRI
 , size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

BASE COUNT 206 a 157 c 179 g 131 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5,978-57 Length: 673
 Score: 1027.00 Matches: 193
 Percent Similarity: 92.86% Conservative: 15
 Best Local Similarity: 86.16% Mismatches: 15
 Query Match: 69.35% Indels: 1
 DB: 13 Gaps: 0

US-09-513-365A-1 (1-280) x BU386788 (1-673)

QY 33 GluCysValGluSerLeuProHis-AspMetGlnArgAenValSerValLeuArgGluLe 52
 Db 2 GAGTGGTGGAGTCTGCTGCGGCTGGACATCCAGGCGCAACGTCGCTGCTGCGGAGGT 61

QY 52 uAspAenLysTyrGlnGlnThrLeuLysGluLeuAspValTyrGluLysTyrLys 72
 Db 62 GCACACCCGGTCCCAAGAAAGCTTTAAAGGAAATAGACGACGCTATGAAAAATACAAGTC 121

QY 72 sGluAspAspLeuAenGlnLysLysArgLeuGlnGlnLeuGlnArgAlaLeuLeuAs 92
 Db 122 TGAGAACCATCTCTGCTCAGAGAAACGCTTGCAGCAGCACCTCCAGCGGGCTTTATCAA 181

QY 92 nSerGlnGlnLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValG 112
 Db 182 CAGTCAAGAACTCGGAGATGAGAAATTCAGATAGTTACTCAGATGCTCGAACTGGTAGA 241

QY 112 uAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerG 132
 Db 242 GAATAGACCCACAGATGGAACACACTCTCAGTGTCTTTCAGGATCTCTCTGAAACCGA 301

QY 132 uArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerArgArgPr 152
 Db 302 CAAGCCTCTGGAAGAGGCGCAAGATGGAGTCTCTGCCAGCCAGAGAGATCATCATCAGTAGACC 361

QY 152 oArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAenGlyLysLys 172
 Db 362 TCGTGGCAGCAACACGAGAGCGGACCTGTGCCATATAGCCACGGATCGATCGA 421

QY 172 pCysAspAspGlnProProLysGluLysLysSerLysSerAlaLysLysLysArgSe 192

Db 422 CTGCGACGATCAGCCACCTAAAGAGAAAAGATCGAAATCTTCCAGAGAAAAACGCTC 481
 Qy 192 rLysAlaLysGlnArgGluAlaSerProValGluPheAlaIleAspProAsnGluPr 212
 Db 482 CAAGGCCAAACAGAGAGGAGGTTTACCCCGTGGAGTTTGGCATTGATCCCAATGAACC 541
 Qy 212 oThrTyCysLeuCysAsnGlnValSerTyGlyGluMetIleGlyCysAspAsnGluGl 232
 Db 542 GACTTACTGTTATTAACCAAGTGCTTACGGGAAATGATAGGATGATTAACGACAC 601
 Qy 232 nCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyLysProLysGlyLy 252
 Db 602 GTGTCTATTAGTGGTTCACCTTCGTGTGTGGACTCACCTATAAACCGAAGGGAA 661
 Qy 252 sTrpTyCys 255
 Db 662 ATGGTATTGC 671

RESULT 12

BM982877/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM982877 735 bp mRNA linear EST 21-FEB-2003
 UI-CF-EN1-acs-d-05-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-acs-d-05-0-UI 3', mRNA sequence.
 BM982877
 BM982877.1 GI:19606826
 EST.

Source Homo sapiens (human)

Organism Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS
 TITLE

Genome Res. 6 (9), 791-806 (1996)
 97044477
 889548

Journal
 MEDLINE
 PUBMED

COMMENT
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source
 Location/Qualifiers
 1..735
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-EN1-acs-d-05-0-UI"
 /tissue_type="Primary Lung Cystic Fibrosis Epithelial
 Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-EN1"
 /notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-EN1 is a normalized cDNA library containing the
 following tissue(s): Primary Lung Cystic Fibrosis
 Epithelial Cells. The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was ligated to an EcoR I adaptor, digested with Not

I, and cloned directionally into pT7T3-Pac vector. The
 oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CTGCTCAGGT.

TAG LiB=UI-CF-EN1

TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS

6hr to LPS 24h

TAG_SEQ=CTGCTCAGGT"

BASE COUNT 180 a 161 c 114 g 280 t

ORIGIN

Alignment Scores:

Pred. No.: 9.93e-57 Length: 735
 Score: 1024.00 Matches: 190
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 69.14% Indels: 0
 DB: 12 Gaps: 0

US-09-513-365A-1 (1-280) x BM982877 (1-735)

Qy 91 IleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeu 110

Db 735 ATTAATAGTCAAGAAATGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTG 676

Qy 111 ValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu 130

Db 675 GTGGAAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTCACAGATCTCTGCTGAA 616

Qy 131 SerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerArg 150

Db 615 AGTGACGAGCTTCAGATAAAGCAAGATGGATTCCAGCCACCAACAGAAAGATCTTCAAGA 556

Qy 151 ArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaSerGlyIle 170

Db 555 AGACCCCGCAGCGAGCGGACAGTGAAGCCGCGTATTTATGTACATGGCAAAATGGGATT 496

Qy 171 GluAspCysAspAspGlnProLysGluLysSerLysSerLysSerAlaLysLysLys 190

Db 495 GAAGACTGTGATGATCAGCCACCTAAAGAAAGAAATCCAAATCAGCAGCAAGAAAGAAA 436

Qy 191 ArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAsn 210

Db 435 CGCTCCAGGCCAACAGAGGAGGAGCTTCACTGTGTGAGTTGCAATAGATCTCTAT 376

Qy 211 GluProThrTyCysLeuCysAsnGlnValSerTyGlyGluMetIleGlyCysAspAsn 230

Db 375 GAACCTACATACCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAGGATGTGACAAT 316

Qy 231 GluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyLysProLys 250

Db 315 GAACAGTGTCCAATTTGAATGGTTTCATCTTTCATGTGTTTACCTTACCTATAAACCAAG 256

Qy 251 GlyLysTrpTyCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThr 270

Db 255 GGGAAATGTTATGTCCTCCAAAGTCCAGGGAGATATAGAGAAACCAATGGCAACAAAGTACT 196

Qy 271 GluLysThrLysLysAspArgSerArg 280

Db 195 GAAAGACAAAAAGGATAGAGATCGAGG 166

RESULT 13

BU323498

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

BU323498 707 bp mRNA linear EST 28-NOV-2002
 603489003F1 CSEQCHN63 Gallus gallus cDNA clone ChEST388e2 5', mRNA
 sequence.

BU323498
 BU323498.1 GI:25831499
 EST.

Source Gallus gallus (chicken)
 Gallus gallus
 ORGANISM

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 707)
Fongman, P. E., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,
Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A., and Hubbard, S. J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)

JOURNAL

22335534

MEDLINE

12445392

PUBMED

COMMENT

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Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

Location/Qualifiers

1..707

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, Hisex"

/db_xref="taxon:9031"

/clone="CHEST388e2"

/dev_stage="36"

/lab_host="DH10B"

/clone_lib="CSECHN63"

/note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
EcORI; Site_2: NotI; this normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntly ligated to NotI adapters, digested with EcORI
, size-selected, and cloned into the NotI and EcORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

BASE COUNT

ORIGIN

205 a 171 c 195 g 136 t

Alignment Scores:

Prod. No.: 1.3e-56 Length: 707
Score: 1022.00 Matches: 195
Percent Similarity: 91.77% Conservative: 17
Best Local Similarity: 84.42% Mismatches: 18
Query Match: 69.01% Indels: 1
DB: 13 Gaps: 0

US-09-513-365A-1 (1-280) x BUS23498 (1-707)

QY 18 GYGLuArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer 37
Db 15 GGGAGCGGGCCCGCTGCTTCGCTAGCTCAGGACTACTGAGTGGGTGGATCG 74
QY 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
Db 75 CTGCGCGTGACATCCAGCGCAACGTCGCTGCTCGGGAGGTGGACACCCGGTGCCAA 134
QY 58 GluThrLeuLys-GluLeuAspValTyrGluLysTyrLysLysLysLysLysLys 77
Db 135 GAAGCTTTAAAGGGAATAGACACGCTCTATGAAATAATCAAGCTCTGAGAACGATCCTGC 194
QY 77 nGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGluLeuGln 97
Db 195 TCAGAGAACCGTTTCAGCAGCAGCAGCTCCAGCGGGCTTTTATCAACAGTCAAGACTTGG 254
QY 97 YAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
Db 255 AGATGAGAAATTCAGATAGTACTCAGATGCTGGAACCTGGTAGAATAGAGCCCGGACA 314

QY 117 nMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLy 137
Db 315 GATGAAACACACTCTCAGTGTTCCTGAGTATCTGCTGAAACACGCAAGCCTCTGCAAAA 374
QY 137 sAlalysMetAspSerSerGlnProGluArgSerArgArgProArgArgGlnArgTh 157
Db 375 GGCCCAAGATGGAGTCTCTCCAGCCAGAGAGATCATCAGCTAGACCTCTGTCGGCAGCAAC 434
QY 157 rSerGluSerArgAspLeuCysHisMetAlaAenGlyIleGluAAspCysAspAspGlnPr 177
Db 435 CAGCCAGAGAGCCCGACCTGTGCTATATAGCCAGGATCGATGATGCTGCGACATCAGCC 494
QY 177 oProLysGluLysLysSerLysSerAlalysLysLysLysLysLysLysLysLysLys 197
Db 495 ACCTAAAGAGAAAGATCGAAATCTTCCAAGAAGAAAGAAAGAAAGAAAGAAAGAAAG 554
QY 197 uArgGluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCy 217
Db 555 GAGGAGAGGTTTCACCCGTGGAGCTTGGGATTCATCCATGAACCGACTTACTGCTTATG 614
QY 217 sAsnGlnValSerTyrGluMetIleGlyCysAspAsnGluGlnCysProIleGluTr 237
Db 615 TAAACAAGTGTCTTACGGCGAAATGATAGGATGTATACGAACGAGTGTCTTATTGAGTG 674
QY 237 pPheHisPheSerCysValSerLeuThrTyr 247
Db 675 GTTCCACTTCTGCTGTAGGACTCACCTAT 705
RESULT 14
BUS91073/3/c
LOCUS
DEFINITION
AGENCOURT 8866651 NIH_MGC_137 Mus musculus cDNA clone IMAGE:6430926
5', mRNA sequence.
BUS91073
BUS91073.1 GI:23242616
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
cDNA Library Preparation: Catherine Lee, Endocrine Pancreas
Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBD11 row: a column: 07
High quality sequence stop: 560.
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/clone="IMAGE:6430926"
/lab_host="DH10B"
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/note="Organ: pancreas; Vector: pSPOR1; Site 1: SalI;
Site 2: NotI; Library consists of a pool of clones
rearrayed from the following libraries: Melton normalized
mixed mouse pancreas 1 NI-MMS1, Amplified Melton mouse
islets 1 Misl-A, and Kaestner ngm3 wt. Clones rearrayed in
the laboratory of K. Kaestner (University of Pennsylvania
). Note: this is a NIH MGC Library."
BASE COUNT 197 a 217 c 161 g 289 t

ORIGIN

Alignment Scores: 1.28e-55 Length: 864
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 Best Local Similarity: 68.03% Indels: 2
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US-09-513-365A-1 (1-280) x BU591073 (1-864)

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 QY 113 nArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluAr 133
 Db 662 CCGAGCGAGACAATCGAGCTGATTCACAGTGTTCAGAGGATCTCTGCTGAAAGTGAGCG 603
 QY 133 gAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerArgProAr 153
 Db 602 AGCCTCAGACCAAGTCGAAGATGATTCAGTCAACCGGAAGATCTTCTAGAAGACCTCG 543
 QY 153 gArgGlnArgThrSerGlnSerArgAspLysCysHisMetAlaAsnGlyIleGluAspCy 173
 Db 542 AAGACAGAGGACCAAGTGAGAGCGGTGACTATGTCATCAGCAACCGGATTCAGCAGTG 483
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 ACCESSION BG184056.1 GI:13705743
 VERSION EST.
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 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 798)
 AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,

Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
 Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
 ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
 ,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL
 MEDLINE
 PUBMED

COMMENT

Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@atersys.com

High quality sequence stop: 531.

Location/Qualifiers

1..798

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/clone_lib="Athersys RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression
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 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

BASE COUNT 197 a 178 c 130 g 293 t

ORIGIN

Alignment Scores:

Pred. No.: 1.4e-55 Length: 798
 Score: 1006.50 Matches: 209
 Percent Similarity: 95.43% Conservative: 0
 Best Local Similarity: 95.43% Mismatches: 10
 Query Match: 67.96% Indels: 6
 DB: 10 Gaps: 0

US-09-513-365A-1 (1-280) x BG184056 (1-798)

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 QY 82 LeuGlnGlnLeuLeuGlnArgAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 101
 Db 740 CTACAGCAGCTTCTCCAGAGAGCACTATTTAT-AGTCAAGAATGGGAGATGAAAAA- 683
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Qy 242 CysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAsp 261
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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1605.030 Million cell updates/sec

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Perfect score: 1481

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1481	100.0	1078	US-09-601-478-7	Sequence 7, Appli
3	1334	90.1	1154	US-09-484-970B-81	Sequence 81, Appli
4	853.5	57.6	873	US-09-006-783A-4	Sequence 4, Appli
5	728	49.2	1902	US-09-258-257-1	Sequence 1, Appli
6	728	49.2	1902	US-09-258-371-1	Sequence 1, Appli
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8	728	49.2	1902	US-08-751-230-1	Sequence 1, Appli
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16	722	48.8	2061	3	US-09-006-783A-2	Sequence 2, Appli
17	662	44.7	633	3	US-09-006-783A-6	Sequence 6, Appli
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19	396.5	26.8	678	3	US-09-195-286-3	Sequence 3, Appli
20	359	24.2	1864	4	US-09-620-312D-435	Sequence 435, App
21	314	21.2	451	4	US-09-370-838-146	Sequence 146, App
22	172.5	11.6	8931	3	US-09-051-019-1	Sequence 1, Appli
23	127.5	8.6	1820	3	US-08-845-258-17	Sequence 17, Appli
24	127.5	8.6	1820	3	US-08-845-258-37	Sequence 37, Appli
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ALIGNMENTS

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; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Ostuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
; FILE REFERENCE: 060193
; CURRENT APPLICATION NUMBER: US/09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
US-09-601-478-6

Alignment Scores:
Pred. No.: 6.8e-156 Length: 840
Score: 1481.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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US-09-513-365A-1 (1-280) x US-09-601-478-6 (1-840)

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Db 181 AAGGAATTTGATGATGCTTACGAAATATTAAGAAAGAGATGATTTAAACCAAGAGAAA 240
QY 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGluLeuGlyAspGluLys 100
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; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/09601478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
; NAME/KEY: CDS
; LOCATION: (92)..(931)
; US-09-601-478-7

Alignment Scores:
Pred. No.: 9,83e-156 Length: 1078
Score: 1481.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-513-365A-1 (1-280) x US-09-601-478-7 (1-1078)

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QY 221 SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluThrPheHisPhe 240
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RESULT 3

US-09-484-970B-81
; Sequence 81, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkumth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 81
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 197886.1CB1
; NAME/KEY: unsure
; LOCATION: 17-37
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-81

Alignment Scores:
Pred. No.: 2,64e-139 Length: 1154
Score: 1334.00 Matches: 270
Percent Similarity: 81.87% Conservative: 1
Best Local Similarity: 81.57% Mismatches: 9
Query Match: 90.07% Indels: 53
DB: 4 Gaps: 1

US-09-513-365A-1 (1-280) x US-09-484-970B-81 (1-1154)

QY 1 MetLeuGlyGlnGlnGlnGlnLeuTySerSerAlaAlaLeuLeuThrGlyGluArg 20
Db 9 ATGTTAGNNNNNNNNNNNNNNNNNNNNCTCGCTCGCTCGCTCGCTCGCGGGAGCG 68
QY 21 SerArgLeuLeuThrCysTyValGlnAspTyLeuGluCysValGlnSerLeuProHis 40
Db 69 AC-CGGCTGCTACCTGCTACGTCGAGGACTCTTGAGTGGCTGGAGTGGCTGCCAC 127
QY 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyGln----- 57
Db 128 GACATGCAGAGGAACGTGCTGTGCTGCGAGA-CTGGACACAAATATCAAGTCGGGC 186
QY 57 ----- 57
Db 187 TGTGCGGGGGCGTGTGTTGCGGCCCGAGAGTCCGAATCGGGTTTGAGCATGTTT 246
QY 57 ----- 57
Db 247 GCGGTGATGTTTCCAACTCTTTCCAGTCAATGATGATGATGATGATGATGATGATGAT 306
QY 58 -----GluThrLeuLysGluLeuAspValTyGlyLysTy 70
Db 307 ACCGTGCGGATCTGCTCGCAACGTTTAAAGGAATGATGATGATGATGATGATGATGAT 366
QY 70 rLysLysGluAspAspLeuGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLe 90
Db 367 TAAGAAAGAGATGATTTAAACAGAGAAACGCTCTACAGCAGCTTCTCCAGAGCACT 426
QY 90 uLeuAsnSerGlnLeuGlyAspGluLysLysLysLysLysLysLysLysLysLysLys 110
Db 427 AATTAATAGTCAAGAAATGGAGATGAAAAATACAGATTGTTTACACAAATGCTCGAAT 486
QY 110 uValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaG 130

Db 487 GGTGAAAAATCGGGCAAGACAAATGAGTTACACTCACAGTGTTCCTCAAGATCCTGCTCA 546
QY 130 uSerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerAr 150
Db 547 AAGTGAACGAGCCTCAGATAAAGCAAGATGATTCAGCCCAACCAAGAAAGATCTTCAAG 606
QY 150 gArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGly 170
Db 607 AAGACCCCGCAGCAGCGGACCGAGTGAAGCCGTGATTTATGTCACATGGCAATGGAT 666
QY 170 eGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLysLysLy 190
Db 667 TGAAGACTGTGATGATCAGCCACCTAAAGAAAAAGAAATCCAAGTCAGCAAGAAAAAGAA 726
QY 190 sArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaLeuAspProAs 210
Db 727 ACGTCCAAAGGCCAAGCAGGAAAGGAAAGCTTCACCTGTGTGAGTTTGCAATAGATCTTAA 786
QY 210 nGluProThrTyrcysLeuCysAsnGlnValSerTyrcysGluMetIleGlyCysAspAs 230
Db 787 TGAACCTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAGGATGTGACAA 846
QY 230 nGluGlnCysProLysGluTyrPheHisPheSerCysValSerLeuThrTyrcysProLy 250
Db 847 TGAACAGTGTCCAATGAAATGTTTTCACCTTTTCATGTGTTTTCATCTTACCTATAAACCAAA 906
QY 250 sGlyLysTyrcysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerTh 270
Db 907 GGGGAAATGTTATGCCAAAGTGCAGGGGAGATATATGAGAAACAAATGACAAAAAGTAC 966
QY 270 rGluLysThrLysLysAspArgSerArg 280
Db 967 TGAAGACAAAAAAGGATAGAGATCGAGG 997

RESULT 4

US-09-006-783A-4
; Sequence 4, Application US/09006783A
; Patent No. 6257366
; GENERAL INFORMATION:
; APPLICANT: Gukov, Andrey V
; APPLICANT: Garkavstev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
; TITLE OF INVENTION: Pathway
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,783A
; FILING DATE: 15-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6297366nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 97,837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 873 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..813
US-09-006-783A-4

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Alignment Scores:

```

Pred. No.: 6,3e-86 Length: 873
Score: 853.50 Matches: 161
Percent Similarity: 75.74% Conservative: 45
Best Local Similarity: 59.19% Mismatches: 51
Query Match: 57.63% Indels: 15
DB: 3 Gaps: 3

```

US-09-513-365A-1 (1-280) x US-09-006-783A-4 (1-873)

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QY 18 GlyGluArgSerArgLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer 37
DB 25 GGGAGCAGCTCCACCTGGTGAAC---TATGGAGAGTACTCTGAGCTCCATCGAGTCC 81
QY 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
DB 82 CTGCTTTTCGACTTCGAGAGAAATGTCTCGTGTGCGGAGAGATCGACGCGAAATACCAA 141
QY 58 GluThrLeuLysGluLeuAspValTyrGluLysTyrLysGluAspLeuAsn 77
DB 142 GAGATCCTGAAGAGCTAGACGAGTCTACGAGCGCTTCAGTCGCGAGACACACGGGCG 201
QY 78 GlnLysLysArgLeuGlnGlnLeuLeuArgAlaLeuLeuAsnSerGlnGluLeuGly 97
DB 202 CAGAAGCGCGGATGCTGACTGTGTGCGAGCGCGCTGATCCGACGCCAGAGCTGGGC 261
QY 98 AspGluLysLeuLeuValThrGlnMetLeuLeuValGluLeuValGluLeuValGlu 117
DB 262 GACGAGAGATCCAGATCTGAGCCAGATGTTGAGAGTGGTGGAGAACCGACGCGGCGAG 321
QY 118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
DB 322 GTGACAGCCACCGTGGAGCTGTTGAGGCGCGACGAGGCTGGGCGACACAGTGGGCAAC 381
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnPro 145
DB 382 AGCGGCAAGTGGCGCGGACAGCCCAATGGCGATGCGGTAGCGGAGCTGTGACAGCCC 441
QY 146 GluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHis 165
DB 442 -----AACAGCAAGCGCTCACGGCGGCGAGCGGCAACACGAGAACCGTGAGAACGGCTCC 495
QY 166 MetAlaAsnGlyLeuGluAspCysAspAspGlnProProLysGluLysLysSerLys 185
DB 496 AGCAACACGACGACGACGCGCGCTCGGGGACACCCCAAGGAGAGAGGCGCAAGACC 555
QY 186 AlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPhe 205
DB 556 TCCAGAGAGAGAGCGCTCCAGGCGCAAGCGCGGAGAGAGCGTCCCTCCCGACCTC 615
QY 206 AlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMet 225
DB 616 CCCATCGACCCCAACGACCCAGCTACTGTCTGTGCAACACGAGTCTCTATGGGAGATG 675
QY 226 IleGlyCysAspAsnGluGlnCysProIleGluTTPheHisPheSerCysValSerLeu 245
DB 676 ATCGGTGGGACCAACAGCAGTGGCCCATCGAGTGGTTCACCTTCCTGCGTGGGGCTC 735
QY 246 ThrTyrLysProLysGlyLysTTPyrCysProLysCysArgGluValAspAsnGluLysThr 265
DB 736 AATCAATAACCCAGGCGCAAGTGGTACTGTCCCAAGTGGCGGGGAGAACGAGAGACC 795
QY 266 MetAspLysSerThrGluLysThrLysLysAspArg 277
DB 796 ATGGACAAAGCCCTCGGAGAAATCCAAAAAGAGAGG 831

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RESULT 5

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US-09-258-257-1
; Sequence 1, Application US/09258257
; Patent No. 5965398
; GENERAL INFORMATION:
; APPLICANT: GARKAVTSEV, Igor
; APPLICANT: RIABOWOL, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 854-7400
; TELEFAX: (650) 854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..738
US-09-258-257-1

```

Alignment Scores:

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Pred. No.: 1,948-71 Length: 1902
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 2 Gaps: 2

```

US-09-513-365A-1 (1-280) x US-09-258-257-1 (1-1902)

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QY 56 TyrGlnGluThrLeuLysGluIleAspValTyrGluLysTyrLysGluAspAsp 75
DB 31 TGGAAACAGACTCTGAGGAGCTAGCAGGTCTACGAGCGCTTCAGTCGCGAGACAGAC 90
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu 95
DB 91 GGGGCGGCAAGAGCGCGGATGTGTGACCTGTGTGCGCGCGCTGTATCCGCGAGGAG 150
QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
DB 151 CTGGGCGGAGAGAAATCCAGATCGTGGAGCCAGATGTTGGAGCTGTGTGAGAACCCACG 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130

```

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Db 211 CGCAGGTGCAGCCAGCTGTTTCAGGGCGCAGCAGGAGTGGCGGCACAGAGT 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 271 GGCAACAGCGCGAAGTTGGCGGCAGACAGCCCAATGGCGATGGGTAGCGCAGTCTGAC 330
QY 144 GlnProGluArgSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
Db 331 AAGCCC-----AACAGCAAGCGCTCACGGCGGCAGCGCAACACGAGAACCGTGAGAAC 384
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysSer 183
Db 385 GCGTCCAGCAACACGACAGCAGCGCGCTCGGCGCACCCCAAGGAGAGAGGCC 444
QY 184 LysSerAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 203
Db 445 AAGACCTCCAGAGAGAGAGCGCTCCAGGCCCAAGCGCGAGAGGGGTCCCTTCC 504
QY 204 GluPheAlaIleAspProAsnGluProThrTyxCysLeuCysAsnGlnValSerTyrgly 223
Db 505 GACCTCCCATCAGCCCAACGACAGCAGCGCGCTCGGCGCACCCCAAGGAGAGAGGCC 564
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisSerCysVal 243
Db 565 GAGATGATCGCTGCGCAGCAACGACGAGTGCCTCATCGAGTGGTTCACATTCCTCGTGG 624
QY 244 SerLeuThrTyrlsProLysGlyLysTyrlsTyrlsTyrlsTyrlsTyrlsTyrls 263
Db 625 GCGCTCAATCATAAACCAAGGCGAAGTGTATCTGTCCCAAGTCCCGGGGGAGAACGAG 684
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 685 AAGACCATGCAACAAAGCCCTGGAGAAATCCAAAAAGAGAGG 726
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RESULT 6

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US-09-258-371-1
; Sequence 1, Application US/09258371
; Patent No. 5986078
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Ribowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,371
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..741
US-09-258-371-1
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Alignment Scores:

```
Pred. No.: 1,94e-71 Length: 1902
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 2 Gaps: 2
```

US-09-513-365A-1 (1-280) x US-09-258-371-1 (1-1902)

```
QY 56 TyrGlnGluThrLeuLysGluIleAspAspValTyrlsTyrlsTyrlsTyrlsTyrlsTyrls 75
Db 31 TGGAAACAGATCCTGAAGGAGCTAGACGAGTGTACGAGCGCTTCAGTCGCGAGACAGAC 90
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuLeuLeuLeuLeu 95
Db 91 GGGCGCGCAGAAAGCGCGGATGCTGCACTGTGTGCGAGCGCGCTGATCCGACCGCAGGAG 150
QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuLeuLeuValGluAsnArgAla 115
Db 151 CTGGGCGCAGAGAAGATCCAGATCGTAGCCAGATGCTGGAGCTGTGGAGAACCGGCACG 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
Db 211 CGCAGGTGGACAGCCACCGTGGAGCTGTTCGAGCGCAGCAGGAGTGGCGGCACAGAGT 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 271 GGCAACAGCGCGAAGTTGGCGGCAGACAGCCCAATGGCGATGCGGTAGCGCAGTCTGAC 330
QY 144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
Db 331 AAGCCC-----AACAGCAAGCGCTCACGGCGGCAGCGCAACACGAGAACCGTGAGAAC 384
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
Db 385 GCGTCCAGCAACACGACAGCAGCGCGCTCGGCGCACCCCAAGGAGAGAGAGGCC 444
QY 184 LysSerAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 203
Db 445 AAGACCTCCAGAGAGAGAGCGCTCCAGGCCCAAGCGCGAGAGGGGTCCCTTCC 504
QY 204 GluPheAlaIleAspProAsnGluProThrTyrlsTyrlsTyrlsTyrlsTyrlsTyrls 223
Db 505 GACCTCCCATCAGCCCAACGACAGCAGCGCGCTCGGCGCACCCCAAGGAGAGAGGCC 564
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisSerCysVal 243
Db 565 GAGATGATCGCTGCGCAGCAACGACGAGTGCCTCATCGAGTGGTTCACATTCCTCGTGG 624
QY 244 SerLeuThrTyrlsProLysGlyLysTyrlsTyrlsTyrlsTyrlsTyrlsTyrlsTyrls 263
Db 625 GCGCTCAATCATAAACCAAGGCGAAGTGTATCTGTCCCAAGTCCCGGGGGAGAACGAG 684
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 685 AAGACCATGCAACAAAGCCCTGGAGAAATCCAAAAAGAGAGG 726
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RESULT 7

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US-08-569-721A-1
; Sequence 1, Application US/08569721A
; Patent No. 6037121
; GENERAL INFORMATION:
; APPLICANT: GARKAVTSEV, Igor
```

```

; APPLICANT: RIABOWOL, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22131-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,721A
; FILING DATE: 08-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 854-8275
; TELEFAX: (650) 854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..738
;
US-08-569-721A-1
Alignment Scores:
Pred. No.: 1,94e-71 Length: 1902
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 3 Gaps: 2

US-09-513-365A-1 (1-280) x US-08-569-721A-1 (1-1902)
QY 56 TyrGlnGluThrLeuLysGluLeuAspValTyrGluLysTyrLysLysGluAspApp 75
Db 31 TGGAAACAGATCTGAAGAGCTAGACGAGTGTCTGCGCGGCTTTCAGTCGCGAGACAGAC 90
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuGlnAlaLeuLeuLeuLeuLeuLeuLeu 95
Db 91 GGGGCCAGACAGCGCGGAGTGTGCACTGTGTGCGAGCGCGCTGTGTCGCGAGGAG 150
QY 96 LeuGlyAspGluLysLeuGlnLeuValThrGlnMetLeuGluLeuValGluAsnArgAla 115
Db 151 CTGGCGCAGCAGAAATCCAGATCGTGTGAGCGAGTGTGTGAGTGTGTGAGAAACGCGACG 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
Db 211 CGGCAGGTGGACAGCCAGCTGTGAGGCTGTGAGGCGCGCAGCAGGAGTGGCGCAGCAGTG 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSer 143
Db 271 GCGCAACAGCGGAGGTTGGCGCGGACAGCCCAATGGCGATGCGGTAGCGAGTCTGAC 330
QY 144 GlnProGluArgSerArgProArgGlnArgGlnArgThrSerGluSerArgAspLeu 163
Db 331 AAGCCC-----AACAGCAACGCGCTCACGCGCGCAGCGCAACACAGAGAACGCTGAGAAC 384

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QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
Db 385 GCGTCCAGCAACACGACGACGCGCTCGGCGCACACCCCAAGGAGAGAGGCGC 444
QY 184 LysSerAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 203
Db 445 AAGACCTCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 504
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 505 GACCTCCCATCGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 564
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal 243
Db 565 GAGATGATCGCTGCGACACGACGAGTGGCCCATCGAGTGGTTCACCTTCTCGTGG 624
QY 244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
Db 625 GGGCTCAATCATAAACCCCAAGGCAAGTGTACTGTCCCAAGTGGCGGGGAGAGACGAG 684
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 685 AAGACCATGGACAAAGCCCTGGAGAAATCCAAAAAAGAGAGG 726

RESULT 8
US-08-751-230-1
; Sequence 1, Application US/08751230
; Patent No. 6117633
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,230
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..741
;
US-08-751-230-1
Alignment Scores:

```



```
Pred. No.: 1,94e-71 Length: 1902
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 3 Gaps: 2

US-09-513-365A-1 (1-280) x US-08-751-230-1 (1-1902)

QY 56 TyrGlnGluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspAsp 75
Db 31 TGGAAACAGATCTGAGAGAGCTAGACGAGTCTACGAGCGCTTACGTCCGAGACAGAC 90
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuLeuSerGlnGlu 95
Db 91 GGGGCGCAGAGCGCGGATGTCGACGTGTGTGTCAGCGCGCTGATCCGACCCAGGAG 150
QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
Db 151 CTGGGCGAGAGAGATCCAGATCGTGAGCCAGATGCTGGAGTGTGGAGAACCCGACG 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
Db 211 CGGAGGTGGACAGCCAGCTGTGGAGGCTGTCGAGGCGCAGCAGAGCTGGGCGACAGTG 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 271 GGCAACAGCGCAAGTTGGCGGACAGCCCAATGGCGATCGGTAGCGCAGTCTGAC 330
QY 144 GlnProGluArgSerSerArgArgProArgGlnArgThrSerGluSerArgAspLeu 163
Db 331 AAGCCC-----AACAGCAAGCGCTCAGCGCGCAGCGCAACCAACGAGAACCGTGAGAAC 384
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProlLysLysSer 183
Db 385 GGTCCAGCAACACAGCAGCAGCGCGCTCGGCGCACCCCAAGAGAGAGAGGCGC 444
QY 184 LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
Db 445 AGACCTCCAGAGAGAGAGCGCTCCAGGCGCAAGCGCGGAGCGGAGCGTCCCTGCC 504
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 505 GACCTCCCATCCAGCCCAACAGAACCCAGCTACTGTGTGCAACCCAGCTCTCTATGG 564
QY 224 GluMetIleGlyCysAspAsnGlnCysProIleGluTrpPheHisPheSerCysVal 243
Db 565 GAGATGATCGGTGCGACACAGCAGAGTCCCATCGAGTGTTCACCTTCTCGTGGTG 624
QY 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
Db 625 GGGCTCAATCATAAACCCAGGCGCAAGTGTACTGTCCCAAGTCCCGGGGGAGAACGAG 684
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 685 AAGACCATGCAAAAGCCCTGGAGAAATCCAAAAAGAGAGG 726
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RESULT 9

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US-09-499-082-1
Sequence 1, Application US/09499082
Patent No. 6143522
GENERAL INFORMATION:
APPLICANT: Helbing, Caren C.
APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
```

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COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US/08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 109..741
US-09-499-082-1
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Alignment Scores:
Pred. No.: 1,94e-71 Length: 1902
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 3 Gaps: 2
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US-09-513-365A-1 (1-280) x US-09-499-082-1 (1-1902)

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QY 56 TyrGlnGluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspAsp 75
Db 31 TGGAAACAGATCTGAGAGAGCTAGACGAGTCTACGAGCGCTTACGTCCGAGACAGAC 90
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuLeuSerGlnGlu 95
Db 91 GGGGCGCAGAGCGCGGATGTCGACGTGTGTGTCAGCGCGCTGATCCGACCCAGGAG 150
QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
Db 151 CTGGGCGAGAGAGATCCAGATCGTGAGCCAGATGCTGGAGTGTGGAGAACCCGACG 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
Db 211 CGGAGGTGGACAGCCAGCTGTGGAGGCTGTCGAGGCGCAGCAGAGCTGGGCGACAGTG 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 271 GGCAACAGCGCAAGTTGGCGGACAGCCCAATGGCGATCGGTAGCGCAGTCTGAC 330
QY 144 GlnProGluArgSerSerArgArgProArgGlnArgThrSerGluSerArgAspLeu 163
Db 331 AAGCCC-----AACAGCAAGCGCTCAGCGCGCAGCGCAACCAACGAGAACCGTGAGAAC 384
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProlLysLysSer 183
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,371
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..900
; US-09-258-371-9

Alignment Scores:
Pred. No.: 2,18e-71 Length: 2061
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 2 Gaps: 2

US-09-513-365A-1 (1-280) x US-09-258-371-9 (1-2061)

QY 56 TyrGlnGluThrLeuLysGluLeuAspValTyrGluLysTyrLysLysGluAspApp 75
Db 190 TGGAAACATCTCTGAAGAGCTAGACGAGTGTCTAGCGGCTTACGTCGAGACAGAG 249
QY 76 LeuAsnGlnLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuLeuSerGlnGlu 95
Db 250 GGGCGCGCAGAAGCGCGGATGTGCTGTGTCAGCGCGCTGATCCGACCGAGGAG 309
QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
Db 310 CTGGCGCAGCAGAAAGATCCAGATCTGTGAGCCAGATGTGTGAGTGTGTGAGAACCCGACG 369
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
Db 370 CGGCAGGTGGACAGCAGCGTGGAGCTGTTCCAGCGCGCAGCAGGAGTGGCGCAGACAGTG 429
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 430 GGCAACAGCGCGCAAGGTGGCGCGGACAGCCCAATGGCGGTAGCGCAGTCTGAC 489
QY 144 GlnProGluArgSerArgProArgGlnArgThrSerGluSerArgAspLeu 163
Db 490 AAGCCCC-----AACHAGCAGCCCTCAGCGCGCAGCGCAACACGAGAACCTGAGAAC 543
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
Db 544 GCGTCCAGCAACACACGACACGACGCGCGCTCGGGACACCCCAAGGAGAGAGGCC 603
QY 184 LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluLalaSerProVal 203
Db 604 AAGACCTCCAAAGAAGAAGACGCTCCAGGCGCAAGCGGAGCGAGCGGTCCCTGCC 663

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QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 664 GACCTCCCATCGACCCCAACGACGACTGTGTGCAACCAAGGCTCTCTATGGG 723
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal 243
Db 724 GAGATGATCGGCTGCGACCAACGACGAGTGCCTCCCATCGAGTGTTCACCTTCTCGTGGTG 783
QY 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
Db 784 GGGCTCAATCATAAACCCCAAGGCGCAAGTGTACTGTCCCAAGTCCCGGGGGAGACGAG 843
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 844 AAGACCATGCAAAAGCCCTGGAGAAATCCAAAAAGAGAGG 885

RESULT 12
US-08-751-230-9
; Sequence 9, Application US/08751230
; Patent No. 6117633
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,230
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..900
; US-08-751-230-9

Alignment Scores:
Pred. No.: 2,18e-71 Length: 2061
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 2 Gaps: 2

US-09-513-365A-1 (1-280) x US-08-751-230-9 (1-2061)

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QY 56 TyrGlnGluThrLeuLysGluLeuAspValTyrGluLysTyrLysLysGluAspAsp 75
Db 190 TGGAAACAGATCTTGAAGAGCTAGACGAGTCTACGAGCGCTTACGTCCGAGACAGAC 249
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnAlaLeuLeuLeuSerGlnGlu 95
Db 250 GGGGGCCAGAGCGGGGATGTGCACCTGTGTGCAGCGCGCTGTATCCGACGAGGAG 309
QY 96 LeuGlyAspGluLysLeuGlnLeuValThrGlnMetLeuLeuValGluLeuAla 115
Db 310 CTGGGGCAGCAGAGATCCAGATCGTGTGAGCCAGATGTGTGTGAGGAGGAGGAG 369
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu 130
Db 370 CGCGAGGTGGACAGCCAGCTGTGTGAGCGCAGCAGGAGGTGGGGCAGCAGAGTG 429
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 430 GGCACAGCGGCAGAGGTTGGCGGACAGCCCAATGGCGATGGGTAGCGAGTCTGAC 489
QY 144 GlnProGluArgSerArgProArgGlnArgThrSerGluSerArgAspLeu 163
Db 490 AAGCCC-----AACAGCAAGCGCTCACGCGCGCAGCGCAACACGAGAACCGTGAGAAC 543
QY 164 CysHisMetAlaAsnGlyLeuGluAspCysAspGlnProProLysGluLysLysSer 183
Db 544 GCGTCCAGCAACACAGCCAGCGCGGCTCGGGCAGCAGCAGGAGTGGGGCAGCAGAGTG 429
QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluAlaArgGluAlaSerProVal 203
Db 604 AAGACTCCAGAGAGAGAGCGCTCCAGGCCAGCGGCGGAGCGAGGCGTCCCTGCC 663
QY 204 GluPheAlaLeuAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 664 GACCTCCCATCAGCCCAAGCAAGCAACCGACTGTCTGTGCAACCGAGTCTCTATGG 723
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluThrPheHisPheSerCysVal 243
Db 724 GAGATGATCGGTGGCAGCAACAGCAGAGTCCCATCGAGTGTTCACCTTCTCGTGGTG 783
QY 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
Db 784 GGGCTCAATCATMAACCCAGGCGCAAGTGTACTGTCCCAAGTCCCGGGGGAGAACGAG 843
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 844 AAGACCATGGACAAGCCCTGGAGAAATCCAAAAAAGAGAGG 885
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RESULT 13

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US-09-499-082-9
; Sequence 9, Application US/09499082
; Patent No. 6143522
; GENERAL INFORMATION:
; APPLICANT: Helbing, Caren C.
; APPLICANT: Riabowol, Karl
; APPLICANT: Johnston, Randall N.
; APPLICANT: Garkavtsev, Igor
; TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/499,082
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,158
; FILING DATE: 27-MAR-1997
; APPLICATION NUMBER: US 08/751230
; FILING DATE: 15-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-854-7400
; TELEFAX: 650-854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..900
; US-09-499-082-9
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Alignment Scores:
Pred. No.: 2,188-71 Length: 2061
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 3 Gaps: 2
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US-09-513-365A-1 (1-280) x US-09-499-082-9 (1-2061)

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QY 56 TyrGlnGluThrLeuLysGluLeuAspValTyrGluLysTyrLysLysGluAspAsp 75
Db 190 TGGAAACAGATCTTGAAGAGCTAGACGAGTCTACGAGCGCTTACGTCCGAGACAGAC 249
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnAlaLeuLeuLeuSerGlnGlu 95
Db 250 GGGGGCCAGAGCGGGGATGTGCACCTGTGTGAGCGCGCTGTATCCGACGAGGAG 309
QY 96 LeuGlyAspGluLysLeuGlnLeuValThrGlnMetLeuLeuValGluLeuAla 115
Db 310 CTGGGGCAGCAGAGATCCAGATCGTGTGAGCGCAGCAGGAGGTGGGGCAGCAGAGTG 369
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu 130
Db 370 CGCGAGGTGGACAGCCAGCTGTGTGAGCGCAGCAGGAGGTGGGGCAGCAGAGTG 429
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 430 GGCACAGCGGCAGAGGTTGGCGGACAGCCCAATGGCGATGGGTAGCGAGTCTGAC 489
QY 144 GlnProGluArgSerArgProArgGlnArgThrSerGluSerArgAspLeu 163
Db 490 AAGCCC-----AACAGCAAGCGCTCACGCGCGCAGCGCAACACGAGAACCGTGAGAAC 543
QY 164 CysHisMetAlaAsnGlyLeuGluAspCysAspGlnProProLysGluLysLysSer 183
Db 544 GCGTCCAGCAACACAGCCAGCGCGGCTCGGGCAGCAGCAGGAGTGGGGCAGCAGAGTG 603
QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluAlaArgGluAlaSerProVal 203
Db 604 AAGACTCCAGAGAGAGAGCGCTCCAGGCCAGCGGCGGAGCGAGGCGTCCCTGCC 663
QY 204 GluPheAlaLeuAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
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Db 664 GACCTCCCATCAGCCACCAACGACGAGTCTGTGTCACAGGCTCTCTATGGG 723
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal 243
Db 724 GAGATGATCGGTCGACACGACGAGTGTCCCATCGAGTGTTCACCTTCTCTGTCGGTG 783
QY 244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
Db 784 GGGCTCAATCAATAACCCCAAGGCAAGTGTCTGTCTCCCAAGTGTCCCGGGGAGAACGAG 843
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 844 AAGACCATGACAAAGCCCTGGAGAAATCCAAAAAGAGAGG 885

RESULT 14

US-09-258-372-9
; Sequence 9, Application US/09258372
; Patent No. 6238918
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,372
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2061 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 16..900

US-09-258-372-9

Alignment Scores:

Pred. No.: 2,18e-71 Length: 2061
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 3 Gaps: 2

US-09-513-365A-1 (1-280) x US-09-258-372-9 (1-2061)

QY 56 TyrGlnGluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspAsp 75
Db 190 TGGAAACAGATCTCTAGGAGCTAGCAGAGTCTACGAGCGCTTCACTCGCAGACAGAC 249
QY 76 LeuAsnGluLysArgLeuGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 95
Db 250 GGGGCGCAGAACCGCGGATGCTGTCAGAGCGCGCTGATCCGACCGCAGGAG 309
QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuLeuLeuValGluLeuAsnAla 115
Db 310 CTGGGCGCAGAGAAGATCCAGATCTGAGCAGAGTGTGGAGCTGTGTGAGAACCCGACG 369
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu 130
Db 370 CGGAGGTGGACAGCCAGCTGTCGAGCGTTCGAGCGCAGCAGAGTGGCGCACAGTG 429
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 430 GGCACAGCGGCAAGGTTGGCGCGCAGACGAGCCCAATGGCGATGCGGTAGCGCAGTCTGAC 489
QY 144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
Db 490 AAGCCC-----AACAGCAAGCGCTCACGCGCGCAGCGCAACACGAGAACCGTGAAGAC 543
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
Db 544 GCGTCCAGCAACACGACGACGACGCGCGCTCGGGGCACACCCCAAGGAGAGAGGCC 603
QY 184 LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
Db 604 AAGACCTCCAGAGAAGAGCGCTCCAGGCGCAAGCGCGAGCGAGAGCGCTCCCTGCGC 663
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 664 GACCTCCCATCGACCCCAACGAGCCAGTGTGTGTGCAACAGGTCTCTATGGG 723
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal 243
Db 724 GAGATGATCGGTCGCGACACGACGAGTGTCCCATCGAGTGTTCACCTTCTCTGCGTG 783
QY 244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
Db 784 GGGCTCAATCAATAACCCCAAGGCAAGTGTCTGTCCCAAGTGTCCCGGGGAGAACGAG 843
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 844 AAGACCATGACAAAGCCCTGGAGAAATCCAAAAAGAGAGG 885

RESULT 15

US-09-159-871-1
; Sequence 1, Application US/09159871A
; Patent No. 6420136
; GENERAL INFORMATION:
; APPLICANT: RIABOWOL, Karl T.
; TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY
; FILE REFERENCE: 028722-181
; CURRENT APPLICATION NUMBER: US/09/159,871A
; CURRENT FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 60/060,138
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: US 09/006,783
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(897)
US-09-159-871-1

61 CGCAGGATGTTAGGCGAGCAGCAGCAACTGTACTCTCGCTCGCTCTCGACCGG 120
Db |||||||
85 CGCAGGATGTTAGGCGAGCAGCAGCAACTGTACTCTCGCTCGCTCTCGACCGG 144
Qy 121 GGAGCGAGCGGCTGCTCACTCTGCTACGCTGCGAGGACTACCTTTGAGTGGGTGAGTGGCT 180
Db 145 GGAGCGAGCGGCTGCTCACTCTGCTACGCTGCGAGGACTACCTTTGAGTGGGTGAGTGGCT 204
Qy 181 GCCCCAGCATGCGAGGAGACGTGCTGCTGCTGCGAGAGCTGCGACACAAATATCAAGA 240
Db 205 GCCCCAGCATGCGAGGAGACGTGCTGCTGCTGCGAGAGCTGCGACACAAATATCAAGA 264
Qy 241 AACGTTAAAGGAAATGATGATGCTACGAGAAATATTAAGAAAGAGATGATTTAAACCA 300
Db 265 AACGTTAAAGGAAATGATGATGCTACGAGAAATATTAAGAAAGAGATGATTTAAACCA 324
Qy 301 GAAGAAACGCTTACAGCAGCTTCTCCAGAGAGCACTAAATTAATAGTCAAGAAATGGGAGA 360
Db 325 GAAGAAACGCTTACAGCAGCTTCTCCAGAGAGCACTAAATTAATAGTCAAGAAATGGGAGA 384
Qy 361 TGAAGAAATACAGATGTTTACACAAATGCTGGAATGGTGGAAATCGGCAAGACAAAT 420
Db 385 TGAAGAAATACAGATGTTTACACAAATGCTGGAATGGTGGAAATCGGCAAGACAAAT 444
Qy 421 GGAGTTACACTCACAGTGTGTTTCAAGATCTGCTGAAAGTGAACGAGCTTCAGATAAGC 480
Db 445 GGAGTTACACTCACAGTGTGTTTCAAGATCTGCTGAAAGTGAACGAGCTTCAGATAAGC 504
Qy 481 AAAGATGGATTCAGGCCAACAGAAAGATCTTCAAGAAAGACCCCGCAGGCGAGCCAG 540
Db 505 AAAGATGGATTCAGGCCAACAGAAAGATCTTCAAGAAAGACCCCGCAGGCGAGCCAG 564
Qy 541 TGAAGCGGTGATTTATGTCATATGGCAATGGGATGGAAGATGTGATGATCAGCCACC 600
Db 565 TGAAGCGGTGATTTATGTCATATGGCAATGGGATGGAAGATGTGATGATCAGCCACC 624
Qy 601 TAAAGAAAGAAATCAAGTCACCAAGAAAGAAAGACCGTCCCAAGCCCAAGCAGAAAG 660
Db 625 TAAAGAAAGAAATCAAGTCACCAAGAAAGAAAGACCGTCCCAAGCCCAAGCAGAAAG 684
Qy 661 GGAAGCTTCACTGTTGAGTTTGCATATGATCTTAATGAACCTTACATCTGCTTATGCAA 720
Db 685 GGAAGCTTCACTGTTGAGTTTGCATATGATCTTAATGAACCTTACATCTGCTTATGCAA 744
Qy 721 CCAAGTGTCTTATGGGAGATGATAGATGTGACATGACATGCTGCTTGAATGATGTT 780
Db 745 CCAAGTGTCTTATGGGAGATGATAGATGTGACATGACATGCTGCTTGAATGATGTT 804
Qy 781 TCACCTTTTCATGTTTCACTTACCTTATAACCAAGGGGAATGGTATGCTCCCAAGTG 840
Db 805 TCACCTTTTCATGTTTCACTTACCTTATAACCAAGGGGAATGGTATGCTCCCAAGTG 864
Qy 841 CAGGGAGATAATGAGAAACAAATGACAAAGTACTGMAAAGACAAAGGATAGAAG 900
Db 865 CAGGGAGATAATGAGAAACAAATGACAAAGTACTGMAAAGACAAAGGATAGAAG 924
Qy 901 ATCAGGATAGTAAAGCCATCCACATTTTAAAGGTTATTTGCTTTTATATATTCGTT 960
Db 925 ATCAGGATAGTAAAGCCATCCACATTTTAAAGGTTATTTGACTATTATATATTCGTT 984
Qy 961 TGCTTTTCAGAAATGTTTATGGGTAAATGATAGACTATGCAATATTTTATCATTA 1020
Db 985 TGCTTTTCAGAAATGTTTATGGGTAAATGATAGACTATGCAATATTTTATCATTA 1044
Qy 1021 GTATTATGTTGTTTAAAGTTGTTGACTTTG 1054
Db 1045 GTATTATGTTGTTTAAAGTTGTTGACTTTG 1078

RESULT 2

US-10-115-899-6

; Sequence 6, Application US/10115899

; Publication No. US20020151025A1

GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human ING1L gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/10/115,899
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
US-10-115-899-6

Query Match 77.6%; Score 838.4; DB 14; Length 840;
Best Local Similarity 99.9%; Pred. No. 2e-190; 1; Indels 0; Gaps 0;
Matches 839; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 68 ATGTAGGCGCAGCAGCAGCAACTGTACTCTCGCTCGCTCTCTCGACCGGAGCGG 127
Db 1 ATGTAGGCGCAGCAGCAGCAACTGTACTCTCGCTCGCTCTCTCGACCGGAGCGG 60
Qy 128 AGCGGCTGCTCACCTGCTACGTCAGAGCACTACCTTGTGCTGAGTGGTGGAGTGGCTGCCCCAC 187
Db 61 AGCGGCTGCTCACCTGCTACGTCAGAGCACTACCTTGTGCTGAGTGGTGGAGTGGCTGCCCCAC 120
Qy 188 GACATGCGAGGAAAGCTGCTGCTGCGAGAGCTGGCAACAAATATCAAGAAAGCTTA 247
Db 121 GACATGCGAGGAAAGCTGCTGCTGCGAGAGCTGGCAACAAATATCAAGAAAGCTTA 180
Qy 248 AAGGAAATGATGATGCTTACGAAATAATAAGAAAGAGATGATTTAAACCAAGAAAG 307
Db 181 AAGGAAATGATGATGCTTACGAAATAATAAGAAAGAGATGATTTAAACCAAGAAAG 240
Qy 308 CGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAAATGGGAGATGAAAG 367
Db 241 CGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAAATGGGAGATGAAAG 300
Qy 368 ATACAGATTTGTACACAAATGCTCGAATTTGGTGGAAATCGGGCAAGACAAATGGAGTTA 427
Db 301 ATACAGATTTGTACACAAATGCTCGAATTTGGTGGAAATCGGGCAAGACAAATGGAGTTA 360
Qy 428 CACTCACAGTGTTCACAGATCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAGATG 487
Db 361 CACTCACAGTGTTCACAGATCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAGATG 420
Qy 488 GATTCAGCAACCAAGAAAGATCTTCAAGAAAGCCCGCAGGAGCGGACCGATGAAAGC 547
Db 421 GATTCAGCAACCAAGAAAGATCTTCAAGAAAGCCCGCAGGAGCGGACCGATGAAAGC 480
Qy 548 CGTGATTTATGTCACATGCAATGGGATTTGAAGACTGTGATGATCAGCCACCTAAAGAA 607
Db 481 CGTGATTTATGTCACATGCAATGGGATTTGAAGACTGTGATGATCAGCCACCTAAAGAA 540
Qy 608 AAGAAATCCAGCTCAGCAAGAAAGAAACGCTCCAGGCCCAAGCAGGAAAGGGAGCT 667
Db 541 AAGAAATCCAGCTCAGCAAGAAAGAAACGCTCCAGGCCCAAGCAGGAAAGGGAGCT 600
Qy 668 TCACCTGTTGAGTTTGCATATAGATCTTAAATGAACCTACATCTGTTATGCAACCAAGTG 727
Db 601 TCACCTGTTGAGTTTGCATATAGATCTTAAATGAACCTACATCTGTTATGCAACCAAGTG 660
Qy 728 TCTTATGGGAGATGATAGGATGTGCAATGAACAGTGTCCCAATGCAATGTTTCTACTTT 787

Db 661 TCTTATGGGAGATGATAGATGTGCAATGAACAGTGTCCAATTGAATGGTTTCACTTT 720
QY 788 TCATGTGTTTCACTTACCTATAAACCAGGGAATGGTATTGCCCAAGTGCAGGGA 847
Db 721 TCATGTGTTTCACTTACCTATAAACCAGGGAATGGTATTGCCCAAGTGCAGGGA 780
QY 848 GATAATGAGAAAACAATGGCAAAAGTACTGAAAAGCAAAAAGGATAGATCGAGG 907
Db 781 GATAATGAGAAAACAATGGCAAAAGTACTGAAAAGCAAAAAGGATAGATCGAGG 840

RESULT 3

US-09-918-995-37033
; Sequence 37033, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37033
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(421)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-37033

Query Match 35.0%; Score 378.4; DB 11; Length 421;
Best Local Similarity 93.8%; Pred. No. 1.8e-80;
Matches 394; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 606 AAAAGAAATCCAAAGTCAAGCAAGAAAGAAAGCGTCCAAAGCCAGCAAGGAAAGGAAAG 665
Db 1 AAAAGAAATCCAAAGTCAAGCAAGAAAGAAAGCGTCCAAAGCCAGCAAGGAAAGGAAAG 60
QY 666 CTTTCACTGTGAGTTTGCATAGATCCTTAATGAACCTACATACCTGTTATGCAACCAAG 725
Db 61 CTTTCACTGTGAGTTTGCATAGATCCTTAATGAACCTACATACCTGTTATGCAACCAAG 120
QY 726 TGTCTTATGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGTTTCACT 785
Db 121 TGTCTTATGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGTTTCACT 180
QY 786 TTTTATGTGTTTCACTTACCTATAAACCAGGGAATGGTATGCCCAAGTGCAGG 845
Db 181 TTTTATGTGTTTCACTTACCTATAAACCAGGGAATGGTATGCCCAAGTGCAGG 240
QY 846 GAGATAATGAGAAAACAATGGCAAAAGTACTGAAAAGCAAAAAGGATAGAAATCGA 905
Db 241 GAGATAATGAGAAAACAATGGCAAAAGTACTGAAAAGCAAAAAGGATAGAAATCGA 300
QY 906 GGTAGTAAAGGCCATCCACATTTTAAAGGTTATTTGTCTTTTATATAATTCGTTGCTT 965
Db 301 GGTAGTAAAGGCCATCCACATTTTAAAGGTTATTTGTCTTTTATATAATTCGTTGCTT 360
QY 966 TCAGAAAATGTTTTAGGTTAAATGCATAGACTATGCAATAATTTTTTAATCAATTAGTATT 1025
Db 361 TCAGAAAATGTTTTAGGTTAAATGCATAGACTATGCAATAATTTTTTAATCAATTAGTATT 420

RESULT 4

US-09-968-653A-4
; Sequence 4, Application US/09968653A

; Publication No. US20030073084A1
; GENERAL INFORMATION:
; APPLICANT: Guckov, Andrey V
; Garkavstev, Igor
; Riabowol, Karl
; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
; Pathway
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/968,653A
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,783A
; FILING DATE: 15-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030073084A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 97,837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 873 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..813
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-968-653A-4

Query Match 22.0%; Score 237.4; DB 11; Length 873;
Best Local Similarity 59.0%; Pred. No. 1.6e-46;
Matches 462; Conservative 0; Mismatches 291; Indels 30; Gaps 2;
QY 145 CTACGTGAGGACTACCTTGAGTGGTGGAGTCCGTCGCCCGCAGCATCGAGGGAACGT 204
Db 48 CTATGTGGAGGACTACCTTGAGTCCATCGAGTCCCTTCGACTTCGAGGAAATGT 107
QY 205 GTCTGTGCTCCAGAGCTGGCAACAAATATCAAGAAACGTTTAAAGGAAATGATGATGT 264
Db 108 CTCGCTGATCGGGAGATCGACGGGAAATACCAGAGATCCTGAAGAGGCTGACGAGTG 167
QY 265 CTACGAAAATATAAGAAAAGAGATGATTTAAACCAGAGAAACGTTCTACAGCAGCTTCT 324
Db 168 CTACGAGCGCTTCAGTCCGCGAGACAGACGGGGCGGAGAGCGCGGATCTGCATGTGT 227
QY 325 CCAGAGAGACTAATAATATAGTCAAGAAATTTGGAGATGAAAAATACAGATTGTTTACA 384
Db 228 GCAGCGCGCTGATCCGCGAGCAGGAGCTGGCGCAGGAGATCCAGATCGTGAGCCA 287
QY 385 AATGCTCGAATTTGGTGGAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTCGA 444
Db 288 GATGTGGAGCTGGTGGAGAACCCGACCGCGGAGGTGGACGCCACGCTGGAGCTGTCCA 347
QY 445 AGATC-----CTGCTGAAAGTGAACGAGCCTCAGATA 476

Db 348 GCGCAGCAGGAGCTGGCGGACACACAGTGGGCAACAGCGGCAAGGTTGGCGGACAGGCG 407
Qy 477 AACCAAGATGGATTCACGACCAACAGAAAGATCTTCAGAGAGACCCCGCAG--CGACG 534
Db 408 CAATGGCGATGCGGTAGCGAGCTGACAAAGCCCAACAGCAAGCGCTCAGCGGCGGACG 467
Qy 535 GACCAAGTGAAGCGCGTGTATTTATGTCAATGGCAATGGGATTTGAAGACTGTGTATGATCA 594
Db 468 CAACACAGAACCGTGTAGAGACCGTCCAGCAACACAGCAGCAGCGCGCTCGGG 527
Qy 595 GCCACCTAAAGAAAGAAATCCAAAGTCAGCAAAAGAAAGAAACGCTCCAAAGGCCAAGCA 654
Db 528 CACACCAAGGAGAAAGGCAAGACCTCAAGAAAGAAAGAGCGCTCCAAAGGCCAAGG 587
Qy 655 GGAAGGGAGCTTCACCTGTGTAGTTTGCATAGATCTTAATGAACCTACACTGCTT 714
Db 588 GGAGCGAGAGGCGTCCCTGCGGACCTCCCATCGACCAACCAACCGTACTGTCT 647
Qy 715 ATGCAACCAAGTCTTTATGGGAGATGATAGATGTGCAATGAACAGTGTCCAATTGA 774
Db 648 GTGCAACAGGCTCTCTATGGGAGATGATCGGCTGGACACAGCAGTGTCCCATCGA 707
Qy 775 ATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAGGGGAAATGGTATTGCC 834
Db 708 GTGGTTTCACTTCTCGTGGTGGGCTCAATATAAACCAAGGGCAAGTGTGTCTGCC 767
Qy 835 AAGTGCAGGGAGATAATGAGAAACAAATGGACAAAGTACTGAAAGACAAAGGA 894
Db 768 CAAAGTCCGGGGGAGACGAGAAAGCAATGGACAAAGCCCTGGAGAAATCCAAAGGA 827
Qy 895 TAG 897
Db 828 GAG 830

RESULT 5
US-09-764-877-3454
; Sequence 3454: Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3454
; LENGTH: 8487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3454
Query Match 17.0%; Score 183.4; DB 10; Length 8487;
Best Local Similarity 57.0%; Pred. No. 5.5e-33;
Matches 395; Conservative 0; Mismatches 266; Indels 32; Gaps 2;
Qy 236 CAAGAAACGTTAAAGGAAATGTATGTCTACGAAAAATATAGAAAGAGATGATTTA 295
Db 6229 CCAGAGATCTGAAGGAGCTAGACGATGTACGAGCGCTTCACTCGGAGACAGCGG 6288
Qy 296 AACCAAGAAACGCTTACAGAGCTTCTCCAGAGAGCTAATTAATAGTCAAGAAATTG 355
Db 6289 GCGCAGAAAGCGGCGGATGCTGCACTGTGTGACGCGCGCTGATCCGACGCCAGGAGCTG 6348
Qy 356 GGAGATGAAATAATACAGATGTTTACACAAATCTCGAATTTGTTGGAATCGGCAAGA 415
Db 6349 GCGCAGAGAAATCAGATCGTGAAGCAGATGTTGAGAGTGTGGAGAACCCGACGCG 6408
Qy 416 CAAATGGATTAACACTCACAGTGTCTTCCAAAGATC----- 449
Db 6409 CAGGTGACAGCCAGCTGGAGCTGTTTCGAGGCGCAGCAGGAGCTGGCGCACACGCGGC 6468

Qy 450 -----CTGCTGAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAAACCA 504
Db 6469 AACACGCGGAGGCTGGCGGACAGGCCCCAAAGCGGAGCGCAGCGAGGCTGACAAAG 6528
Qy 505 AAGATCTTTCAAGAAAGCCCGCAGCAGCGGACCAAGTGAAGAACCCGTTATGTACAT 564
Db 6529 CCCAACAGCAAG-CGCTCAGGCGGACGCGCAACCAACGAGAACCCGTGAGAACGCGTCCAG 6587
Qy 565 GCGAATGGGATTGAAGACTGTGATGATCAGCCACTTAAGAAAGAAATCCAAAGTCAGC 624
Db 6588 CAACACAGCAGCAGCAGCGCGCTCCGGGCAACCCCAAGGAGAAAGGCGCAAGACCTC 6647
Qy 625 AAGAAAAAGAAACCTCCAAAGCCAAAGCAGGAAAGGAAAGCTTCACCTGTTGAGTTTCG 684
Db 6648 CAAAGAAAGAAAGCCCTCAAGGCCAAGCGGAGGAGGAGGCTCCCTCCGACCTCCC 6707
Qy 685 AATAGATCTTATGAACCTACATACCTATGTTATGCAACCAAGTGTCTTATGGGAGATGAT 744
Db 6708 CATCGACCCCAAGAACCCACGTAAGTGTGTGCAACCAAGGCTCTCTATGGGAGATGAT 6767
Qy 745 AGGATGTGACAAATGAACAGTGTCCAAATGAATGGTTTCACTTTTTCATGTTTTCATTAC 804
Db 6768 CGGCTGCGACACGACGAGTGCCTCCATCGAGTGTTCACCTTCTCGTGGGCTCAA 6827
Qy 805 CTATAAACCAAGGGGAAATGGTATTGCCAAAGTGCAGGGGAGAGATAATGAGAAACAAT 864
Db 6828 TCATAAACCAAGGGCAAGTGTACTGTCCAAAGTGCAGGGGAGAGAACGAGAACCAT 6887
Qy 865 GCACAAAAGTACTGAAAAAGACAAAAAGGATAG 897
Db 6888 GCACAAAGCCCTGGAGAAATCCAAAAAGAGAG 6920

RESULT 6
US-09-968-653A-2
; Sequence 2: Application US/09968653A
; Publication No. US20030073084A1
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrey V
; Garkavstev, Igor
; Riabowol, Karl
; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/968,653A
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,783A
; FILING DATE: 15-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030073084A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 97,837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

RESULT 8

US-10-117-722-435

; Sequence 435, Application US/10117722

; Publication No. US20030219744A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 784CIP28CIP

; CURRENT APPLICATION NUMBER: US/10/117,722

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: 09/620,312

; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1104

; SOFTWARE: pt_FL_genes Version 1.0

; SEQ ID NO 435

; LENGTH: 1864

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (164)..(1420)

US-10-117-722-435

Query Match

Best Local Similarity 8.5%; Score 91.6; DB 13; Length 1864;

; Sequence 435, Application US/10037270

; Publication No. US20030104529A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yunqing

; APPLICANT: Wang, Dunrui

RESULT 9

US-10-037-270-435

; Sequence 435, Application US/10037270

; Publication No. US20030104529A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yunqing

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: Tillinghast, John

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 784CIP28

; CURRENT APPLICATION NUMBER: US/10/037,270

; CURRENT FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1104

; SOFTWARE: pt_FL_genes Version 1.0

; SEQ ID NO 435

; LENGTH: 1864

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (164)..(1420)

US-10-037-270-435

Query Match

Best Local Similarity 8.5%; Score 91.6; DB 15; Length 1864;

; Sequence 146, Application US/09738973

; Patent No. US20020110563A1

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Fling, Steven P.

; APPLICANT: Mohamath, Raodoh

; APPLICANT: Algate, Paul A.

; APPLICANT: Secrist, Heather

; APPLICANT: Indirias, Carol Yoseph

; APPLICANT: Benson, Darin R.

; APPLICANT: Elliot, Mark

; APPLICANT: Mannion, Jane

; APPLICANT: Kalos, Michael D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; FILE REFERENCE: 210121.475C9

; CURRENT APPLICATION NUMBER: US/09/738,973

; CURRENT FILING DATE: 2000-12-14

; NUMBER OF SEQ ID NOS: 587

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 146

; LENGTH: 451

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-738-973-146

Query Match 7.7%; Score 83.6; DB 10; Length 451;
Best Local Similarity 58.6%; Pred. No. 7.3e-10;
Matches 163; Conservative 0; Mismatches 114; Indels 1; Gaps 1;
QY 169 CGTGGAGTCCTGCCCCACACATGACAGAGAACTGTCTGTCTGCGAGAGCTGGACAA 228
Db 16 CATCGAGTCCTCCCTTTCGACTTGCAGAGAAATGTCTCGCTGATCGGGAGATCGACGC 75
QY 229 CAAATATCAAGAAACGTTAAAGGAAATGTATGTCTACGAAATATATAGAAAGA 288
Db 76 GAATACCAAGAGATCTTGAGAGAGCTAGACGAGTGTACAGCGCTTCACTCGCGAGAC 135
QY 289 TGATTTAAACCAAGAAACGTTACAGCAGCTTCTCCAGAGACCACTAATTAATAGTCA 348
Db 136 AGACGGGGCGCAGAGCGGGGATGTCTGCTGTGTCAGCGCGCTGATCCGCA-CCA 194
QY 349 AGAATTGGGAGATGAAAAATACAGATTGTACAAATCTCGAATTTGGTGAATAATCG 408
Db 195 GGAGCTGGGGCGACGAGAAATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCG 254
QY 409 GCGAAGACAAATGGAGTTACACTCACAGTGTTCCTCAAG 446
Db 255 CACGGCGCAGGTGGACAGCCACGTGGAGCTGTTTCGAGG 292

RESULT 11
US-09-854-133-146
; Sequence 146, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-146

Query Match 7.7%; Score 83.6; DB 10; Length 451;
Best Local Similarity 58.6%; Pred. No. 7.3e-10;
Matches 163; Conservative 0; Mismatches 114; Indels 1; Gaps 1;
QY 169 CGTGGAGTCCTGCCCCACACATGACAGAGAACTGTCTGTCTGCGAGAGCTGGACAA 228
Db 16 CATCGAGTCCTCCCTTTCGACTTGCAGAGAAATGTCTCGCTGATCGGGAGATCGACGC 75
QY 229 CAAATATCAAGAAACGTTAAAGGAAATGTATGTCTACGAAATATATAGAAAGA 288
Db 76 GAATACCAAGAGATCTTGAGAGAGCTAGACGAGTGTACGAGCGCTTCACTCGCGAGAC 135
QY 289 TGATTTAAACCAAGAAACGTTACAGCAGCTTCTCCAGAGACCACTAATTAATAGTCA 348
Db 136 AGACGGGGCGCAGAGCGGGGATGTCTGCTGTGTCAGCGCGCTGATCCGCA-CCA 194
QY 349 AGAATTGGGAGATGAAAAATACAGATTGTACAAATCTCGAATTTGGTGAATAATCG 408
Db 195 GGAGCTGGGGCGACGAGAAATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCG 254
QY 409 GCGAAGACAAATGGAGTTACACTCACAGTGTTCCTCAAG 446
Db 255 CACGGCGCAGGTGGACAGCCACGTGGAGCTGTTTCGAGG 292

RESULT 12
US-10-144-649A-146
; Sequence 146, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Ligu
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-144-649A-146

Query Match 7.7%; Score 83.6; DB 15; Length 451;
Best Local Similarity 58.6%; Pred. No. 7.3e-10;
Matches 163; Conservative 0; Mismatches 114; Indels 1; Gaps 1;
QY 169 CGTGGAGTCCTGCCCCACACATGACAGAGAACTGTCTGTCTGCGAGAGCTGGACAA 228
Db 16 CATCGAGTCCTCCCTTTCGACTTGCAGAGAAATGTCTCGCTGATCGGGAGATCGACGC 75
QY 229 CAAATATCAAGAAACGTTAAAGGAAATGTATGTCTACGAAATATATAGAAAGA 288
Db 76 GAATACCAAGAGATCTTGAGAGAGCTAGACGAGTGTACGAGCGCTTCACTCGCGAGAC 135
QY 289 TGATTTAAACCAAGAAACGTTACAGCAGCTTCTCCAGAGACCACTAATTAATAGTCA 348
Db 136 AGACGGGGCGCAGAGCGGGGATGTCTGCTGTGTCAGCGCGCTGATCCGCA-CCA 194
QY 349 AGAATTGGGAGATGAAAAATACAGATTGTACAAATCTCGAATTTGGTGAATAATCG 408
Db 195 GGAGCTGGGGCGACGAGAAATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCG 254
QY 409 GCGAAGACAAATGGAGTTACACTCACAGTGTTCCTCAAG 446
Db 255 CACGGCGCAGGTGGACAGCCACGTGGAGCTGTTTCGAGG 292

RESULT 13
US-09-801-368-257
; Sequence 257, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2004, 16:38:42 ; Search time 93 Seconds
(without alignments)
5125.740 Million cell updates/sec

Title: US-09-513-365A-2
Perfect score: 1080
Sequence: 1 gggccgcgcgcggtgcatg.....aaaaaaaaaaaaaaaaaa 1080

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1046	96.9	1078	4	US-09-601-478-7
2	838.4	77.6	840	4	US-09-601-478-6
3	825.2	76.4	1154	4	US-09-484-970B-81
4	237.4	22.0	873	3	US-09-006-783A-4
5	183.8	17.0	1902	2	US-09-258-257-1
6	183.8	17.0	1902	2	US-09-258-371-1
7	183.8	17.0	1902	3	US-08-569-721A-1
8	183.8	17.0	1902	3	US-08-751-230-1
9	183.8	17.0	1902	3	US-09-499-082-1
10	183.8	17.0	1902	3	US-09-258-372-1
11	183.8	17.0	2061	2	US-09-258-371-9
12	183.8	17.0	2061	3	US-08-751-230-9
13	183.8	17.0	2061	3	US-09-499-082-9
14	183.8	17.0	2061	3	US-09-258-372-9
15	182.2	16.9	2061	3	US-09-006-783A-2
16	182.2	16.9	2061	4	US-09-159-871-1
17	174.4	16.1	633	3	US-09-006-783A-6
18	95.6	8.9	678	3	US-09-195-286-3
19	95.6	8.9	699	3	US-09-195-286-2
20	91.6	8.5	1864	4	US-09-620-312D-435
21	83.6	7.7	451	4	US-09-370-838-146
22	72.4	6.7	7218	1	US-08-232-463-14
23	50.6	4.7	860	1	US-07-847-010-18
24	49	4.5	593	3	US-09-385-982-262
25	46.8	4.3	6124	4	US-08-213-419B-3
26	46.2	4.3	1189	1	US-07-781-034-4
27	46.2	4.3	1189	5	PCT-US92-08328-4

28	45.8	4.2	19124	2	US-08-487-826B-13	Sequence 13, Appl
29	43.8	4.2	1664976	4	US-08-916-421B-1	Sequence 1, Appl
30	43.8	4.1	2327	4	US-09-852-067-1	Sequence 1, Appl
31	43.8	4.1	3489	2	US-08-728-323A-1	Sequence 1, Appl
32	43.8	4.1	3489	4	US-09-298-568-1	Sequence 1, Appl
33	43.8	4.1	3489	4	US-09-410-369-1	Sequence 1, Appl
34	43.8	4.1	32207	2	US-08-770-379-20	Sequence 20, Appl
35	43.8	4.1	32207	3	US-08-757-669A-20	Sequence 20, Appl
36	43.8	4.1	32207	4	US-09-230-371A-20	Sequence 20, Appl
37	43.4	4.0	1147	1	US-08-665-716-1	Sequence 1, Appl
38	43.2	4.0	3625	3	US-09-208-742-3	Sequence 3, Appl
39	43	4.0	1286	4	US-09-489-847-124	Sequence 124, App
40	43	4.0	1342	4	US-09-489-847-89	Sequence 89, Appl
41	43	4.0	3483	4	US-09-130-491-3	Sequence 3, Appl
42	42.8	4.0	603	3	US-09-385-982-251	Sequence 251, App
43	42.8	4.0	774	3	US-08-956-307B-12	Sequence 12, Appl
44	42.8	4.0	778	3	US-08-956-307B-11	Sequence 11, Appl
45	42.8	4.0	3377	6	5198345-16	Patent No: 5198345

ALIGNMENTS

RESULT 1
US-09-601-478-7
; Sequence 7, Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Oetuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGLL gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
; NAME/KEY: CDS
; LOCATION: (92)..(931)
US-09-601-478-7

Query Match	96.9%	Score	1046	DB	4	Length	1078
Best Local Similarity	99.5%	Pred. No.	4.4e-264				
Matches	1049	Conservative	0	Mismatches	5	Indels	0
						Gaps	0
QY	1	GGGCGCGCGCGGTCATGTCGGCTGCGGTCGATGCGGAGCGCGCGCGCGCGGAT	60				
Db	25	GGGCGCGCGCGGTCATGTCGGCTGCGGTCGATGCGGAGCGCGCGCGCGGAT	84				
QY	61	CGGCGAGGTGTAGGCGAGCAGCAGCACTGTACTCGTGGCTGCGCTCTGACCGG	120				
Db	85	CGGCGAGGTGTAGGCGAGCAGCAGCACTGTACTCGTGGCTGCGCTCTGACCGG	144				
QY	121	GGAGCGGCGCGGCTGCTCACCTGTCTGTCGAGGACTACCTTGTAGTGGTGGAGT	180				
Db	145	GGAGCGGCGCGGCTGCTCACCTGTCTGTCGAGGACTACCTTGTAGTGGTGGAGT	204				
QY	181	GGCCACGACATGCAGAGAACTGTCTGTCTGTCGAGGACTGAGCAACAATATCA	240				
Db	205	GGCCACGACATGCAGAGAACTGTCTGTCTGTCGAGGACTGAGCAACAATATCA	264				
QY	241	AACGTTAAAGGAAATGATGTCCTACGAAAAATATAAGAAAGAGATGATTAAAC	300				

see int'l
Filing date

Db 265 AACGTTAAAGGAAATGATGATGTCACGAAAAATATAAGAAAGAGATGATTTAAACCA 324
Qy 301 GAAGAACGCTACAGACGCTTCCAGAGAGACCTAAATTAATAGTCAAGAAATGGGAGA 360
Db 325 GAAGAACGCTACAGACGCTTCCAGAGAGACCTAAATTAATAGTCAAGAAATGGGAGA 384
Qy 361 TGAAGAAATACAGATGTTTACACAAATGCTCGAATTTGGTGGAAAAATCGGCAAGACAAAT 420
Db 385 TGAAGAAATACAGATGTTTACACAAATGCTCGAATTTGGTGGAAAAATCGGCAAGACAAAT 444
Qy 421 GGAGTTACACTACAGGTTTTCAAGATCTCTGCTGAAAGTGAACGAGCCCTCAGATAAAGC 480
Db 445 GGAGTTACACTACAGGTTTTCAAGATCTCTGCTGAAAGTGAACGAGCCCTCAGATAAAGC 504
Qy 481 AAGATGGATTCCAGCCCAACAGAAAGATCTTCAAGNAGACCCCGCAGGCGGACCCAG 540
Db 505 AAGATGGATTCCAGCCCAACAGAAAGATCTTCAAGNAGACCCCGCAGGCGGACCCAG 564
Qy 541 TGAAGCCGCTGATTTATGTCACATGGCAATGGATTTGAAGACTGTGATGATCAGCCACC 600
Db 565 TGAAGCCGCTGATTTATGTCACATGGCAATGGATTTGAAGACTGTGATGATCAGCCACC 624
Qy 601 TAAAGAAAAGAAATCCAAGTCAGCAAGAAAAAGAAACGCTCCAAGGCCCAAGCAGAAAG 660
Db 625 TAAAGAAAAGAAATCCAAGTCAGCAAGAAAAAGAAACGCTCCAAGGCCCAAGCAGAAAG 684
Qy 661 GGAAGCTTCACTGTTGAGTTTGCATAGATCTTAATGACCTACATCTGCTTATGCCAA 720
Db 685 GGAAGCTTCACTGTTGAGTTTGCATAGATCTTAATGACCTACATCTGCTTATGCCAA 744
Qy 721 CCAAGTGTCTTATGGGGAGATGATAGGATGTGACAAATGAACAGTGTCCAATTCGAATGGTT 780
Db 745 CCAAGTGTCTTATGGGGAGATGATAGGATGTGACAAATGAACAGTGTCCAATTCGAATGGTT 804
Qy 781 TCATTTTTCATGTTTTCATCTACCTATATAACCAAGGGGAATGGTATTTGCCAAAGTG 840
Db 805 TCATTTTTCATGTTTTCATCTACCTATATAACCAAGGGGAATGGTATTTGCCAAAGTG 864
Qy 841 CAGGGAGATATGAGAAACATGACAAAGACTGACAAAGTCTGAAAGACAAAAAGATAGAG 900
Db 865 CAGGGAGATATGAGAAACATGACAAAGACTGACAAAGTCTGAAAGACAAAAAGATAGAG 924
Qy 901 ATGAGGTAGTAAGGCGCATCCACATTTTAAAGGGTTATTTGCTTTTATATATTCGTT 960
Db 925 ATGAGGTAGTAAGGCGCATCCACATTTTAAAGGGTTATTTGCTTTTATATATTCGTT 984
Qy 961 TGCTTTTCAGAAATGTTTTAGGGTAAATGCATAAGACTATGCAATATTTTATATCATTA 1020
Db 985 TGCTTTTCAGAAATGTTTTAGGGTAAATGCATAAGACTATGCAATATTTTATATCATTA 1044
Qy 1021 GTATTATGTTGTTTAAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1054
Db 1045 GTATTATGTTGTTTAAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1078

RESULT 2

US-09-601-478-6
; Sequence 6, Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
US-09-601-478-6

Query Match 77.6%; Score 838.4; DB 4; Length 840;
Best Local Similarity 99.9%; Pred. No. 7,9e-210;
Matches 839; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 68 ATGTTAGGCGCAGCAGCAGCAGCAACTGTACTGTCTGGCTGCGCTCTCTGACCGGGAGCGG 127
Db 1 ATGTTAGGCGCAGCAGCAGCAGCAACTGTACTGTCTGGCTGCGCTCTCTGACCGGGAGCGG 60
Qy 128 AGCCGGCTCTCACTGTCTAAGTGAGGACTCTCTTTGAGTGGTGGAGTGGTGGTGGTGGTGG 187
Db 61 AGCCGGCTCTCACTGTCTAAGTGAGGACTCTCTTTGAGTGGTGGAGTGGTGGTGGTGGTGG 120
Qy 188 GACATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 247
Db 121 GACATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Qy 248 AAGGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 307
Db 181 AAGGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
Qy 308 CQTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAAATGGGAGATGAAAAA 367
Db 241 CQTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAAATGGGAGATGAAAAA 300
Qy 368 ATACAGATGTTTACCAAAATGCTCGAATTTGGTGGAAAAATCGGGCAAGACAAATGGAGTTA 427
Db 301 ATACAGATGTTTACCAAAATGCTCGAATTTGGTGGAAAAATCGGGCAAGACAAATGGAGTTA 360
Qy 428 CACTCACAGTGTCTCAAGATCTCTGAAAGTGAACGAGCCTCAGATAAAGCAAGATG 487
Db 361 CACTCACAGTGTCTCAAGATCTCTGAAAGTGAACGAGCCTCAGATAAAGCAAGATG 420
Qy 488 GATTCCAGCAACCAAGAAAGATCTTCAAGAAAGCCCGCAGGCGGACCAAGTGAAGC 547
Db 421 GATTCCAGCAACCAAGAAAGATCTTCAAGAAAGCCCGCAGGCGGACCAAGTGAAGC 480
Qy 548 CQTGATTTATGTCACATGCGAAATGGGATTTGAAGACTGTGATGATCAGCCACCTAAGAA 607
Db 481 CQTGATTTATGTCACATGCGAAATGGGATTTGAAGACTGTGATGATCAGCCACCTAAGAA 540
Qy 608 AAGAAATCCAGTTCAGCAAGAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAGCT 667
Db 541 AAGAAATCCAGTTCAGCAAGAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAGCT 600
Qy 668 TCACCTGTTGAGTTTGCATAGATCCTAATGAACCTACATCTGCTTTATGCAACCAAGTG 727
Db 601 TCACCTGTTGAGTTTGCATAGATCCTAATGAACCTACATCTGCTTTATGCAACCAAGTG 660
Qy 728 TCTTATGGGAGATGATAGGATGTCACATGAACAGTGTCCCAATTCGAATGGTTTCACTTT 787
Db 661 TCTTATGGGAGATGATAGGATGTCACATGAACAGTGTCCCAATTCGAATGGTTTCACTTT 720
Qy 788 TCATGTTGTTTCACTTACCTATATAACCAAGGGGAAATGGTATTTGCCCAAGTGCAGGGA 847
Db 721 TCATGTTGTTTCACTTACCTATATAACCAAGGGGAAATGGTATTTGCCCAAGTGCAGGGA 780
Qy 848 GATAATGAGAAACAAATGGACAAAAAGTACTGAAAAAGACAAAAAGGATGAAGATCGAGG 907
Db 781 GATAATGAGAAACAAATGGACAAAAAGTACTGAAAAAGACAAAAAGGATGAAGATCGAGG 840

RESULT 3

US-09-484-970B-81
; Sequence 81, Application US/09484970B
; Patent No. 6426186

LOCATION: 109..738
US-08-569-721A-1

Query Match 17.0%; Score 183.8; DB 3; Length 1902;
Best Local Similarity 57.0%; Pred. No. 2.2e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;

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QY 237 AAGAAAGCTTAAAGGAAATTTGATGCTCTACCAAAATATTAAGAAAGATGATTTAA 296
DB 35 AACAGATCTTGAAGGAGCTAGACAGTGCTACAGCGCTTCAGTCGCGACAGACGGGG 94
QY 297 ACCAGAAGAAACGCTTACAGCAGCTTCTCCAGAGAGCAGCTAATTAATAGTCAAGAAATGG 356
DB 95 CGCAGAAGCGCGGAGTCTGCACTGTGTGCGAGCGCGCTGATCCGACGACGAGAGCTGG 154
QY 357 GAGATGAAGAAATACAGATTTGTACAAATGCTCGAAATGTTGGTGGAAATTCGGGCAAGAC 416
DB 155 GCAGCAGAGAAGATCCAGATCGTAGGCGAGATGTTGGAGCTGTTGGAGAACCGCACGCGG 214
QY 417 AATGAGTTTACACTCACAGTGTTCAGATC----- 449
DB 215 AGTGGACAGCCAGCTGGAGCTGTTGAGCGCGAGAGAGCTGGGCGACACAGTGGGCA 274
QY 450 -CTGCTCAAGAGTGAACGAGCTTACAGATAAAGCAAGATGATTCAGCCAAACAGAAAGA 508
DB 275 ACAGCGCAAGGTTGGCGCGACAGGCCCAATGCGGATGCGGTAGCGAGTCTGACAAGC 334
QY 509 TCTTCAAGAA--GACCCCGCAGCGAGCGGAGCTTCACTGTTTGAATTTGCGCA 686
DB 335 CCAACAGCAAGCGCTCCAGGCCGAGCGGCAACCAAGCAAGACCGTGAGAACCGCTCCAGCA 394
QY 567 CAATGGGATTTAAGAGCTGTGATGATCAGCCACCTTAAAGAAAGAAATCAAGTCAGCAA 626
DB 395 ACCACGACCAACGACGCGGCTCGGCGACACCCCAAGAGAGAGGCGCAAGACCTCCA 454
QY 627 AGAAAAAGAAACGCTCCAAAGCCAGCAGAGAAAGGAGCTTCACTGTTGATTTGCGCA 686
DB 455 AGAAGAGAAAGCGCTCCAAGGCCAAGCGGAGAGAGCGTCCCTGCGGAGATGATCG 574
QY 747 GATGTGACATGAACGAGTGTCCAAATGAAATGTTTCACTTTTCACTGTTTCACTTACCT 806
DB 575 GCTGCGACACGACGAGTGTCCCAATGAAATGTTTCACTTTTCACTGTTTCACTTACCT 806
QY 807 ATAAACCAAGGGGAAATGTTATTTGCCAAAGTGCAGGGGAGAGATAATGAGAAACAAATGG 866
DB 635 ATAAACCAAGGGCAAGTGTACTGTCTCCCAAGTGTCCGCGGAGAGACGAGACCAATGG 694
QY 867 ACAAAGTACTGAAAGACAAAAAGAGATAG 897
DB 695 ACAAGCGCTGGAGAAATCCAAAAAGAGAG 725
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RESULT 8

US-08-751-230-1
Sequence 1, Application US/08751230
Patent No. 6117633

GENERAL INFORMATION:

APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Kari
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 109..741
US-08-751-230-1

Query Match 17.0%; Score 183.8; DB 3; Length 1902;

Best Local Similarity 57.0%; Pred. No. 2.2e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;

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QY 237 AAGAAACGTTAAAGGAAATTTGATGCTCTACGAAAAATATTAAGAAAGATGATTTAA 296
DB 35 AACAGATCTTGAAGGAGCTAGACAGTGCTACAGCGCTTCAGTCGCGACAGACGGGG 94
QY 297 ACCAGAAGAAACGCTTACAGCAGCTTCTCCAGAGAGCAGCTAATTAATAGTCAAGAAATGG 356
DB 95 CGCAGAAGCGCGGAGTGTGCACTGTGTGCGAGCGCGCTGATCCGACGACGAGAGCTGG 154
QY 357 GAGATGAAGAAATACAGATTTGTACAAATGCTCGAAATGTTGGTGGAAATTCGGGCAAGAC 416
DB 155 GCGACGAGAGATCCAGATCGTGAGCCAGATGTTGAGCTGTGTGAGAACCGCACGCGGC 214
QY 417 AATGGAGTTTACACTCACAGTGTTCAGATC----- 449
DB 215 AGTGGACAGCCAGCTGGAGCTGTTGAGCGCGAGAGAGCTGGGCGACACAGTGGGCA 274
QY 450 -CTGCTGAAAGTGAACGAGCTTACAGATAAAGCAAGATGATTCAGCCAAACAGAAAGA 508
DB 275 ACAGCGGCAAGGTTGGCGCGACAGGCCCAATGCGGATGCGGTAGCGAGTCTGACAAGC 334
QY 509 TCTTCAAGAA--GACCCCGCAGCGAGCGGAGCTTCACTGTTTGAATTTTATGTCAATGG 566
DB 335 CCAACAGCAAGCGCTCACGGCGGAGCGGCAACCAAGAGAACCGTGAGAACCGGCTCCAGCA 394
QY 567 CAATGGGATTTAAGAGCTGTGATGATCAGCCACCTTAAAGAAAGAAATCAAGTCAGCAA 626
DB 395 ACCACGACCAACGACGCGGCTCGGCGACACCCCAAGAGAGAGGCGCAAGACCTCCA 454
QY 627 AGAAAAAGAAACGCTCCAAAGCCAGCAGAGAAAGGAGCTTCACTGTTGATTTGCGCA 686
DB 455 AGAAGAGAAAGCGCTCCAAGGCCAAGCGGAGAGAGCGTCCCTGCGGAGATGATCG 514
QY 687 TAGATCCTTAATGAACCTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAG 746
DB 515 TCGACCCCAACGAAACCAAGCTGCTGTGTGCAACAGAGTCTCTTATGGGAGATGATCG 574
QY 747 GATGTGACAAATGAACAGTGTCCAAATGAAATGTTTCACTTTTCACTTACCTTACCT 806
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Db 575 GCTGCGACACGACGAGTGTCCCATCAGTGGTTCCACTTCTCGTGGGGCTCAATC 634
QY 807 ATAAACCAAGGGAATGTATTGCCCCAAAGTGCAGGGGAGAGATAATGAGAAAACAAATGG 866
Db 635 ATAAACCAAGGCAAGTGTACTGTCTCCCAAGTGTCCCGGGGAGACGAGACCATGG 694
QY 867 ACAAAGTACTGAAAGACAAAAAGGATAG 897
Db 695 ACAAGCCCTGGAGAAATCCAAAAAGAGAG 725

RESULT 9

US-09-499-082-1
; Sequence 1, Application US/09499082
; Patent No. 6143522
; GENERAL INFORMATION:
; APPLICANT: Helbing, Caren C.
; APPLICANT: Riabowol, Karl
; APPLICANT: Johnston, Randall N.
; APPLICANT: Garkavtsev, Igor
; TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/499,082
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,158
; FILING DATE: 27-MAR-1997
; APPLICATION NUMBER: US 08/751230
; FILING DATE: 15-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-854-7400
; TELEFAX: 650-854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..741
US-09-499-082-1

Query Match 17.0%; Score 183.8; DB 3; Length 1902;
Best Local Similarity 57.0%; Pred. No. 2.2e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;
QY 237 AGAAGCGTTAAAGGAAATGTATGCTTACGAAATAAAGAAAGATGATTAA 296
Db 35 AACAGATCTCTGAAGGAGTAGACGAGTGCTTACGAGGCGCTTCAGTCGCGAGACAGACGGGG 94

QY 297 ACCAGAGAAAACGTCTTACAGCAGCTTCTCCAGAGACACTAATAATAGTCAAGAAATTGG 356
Db 95 CGCAGAAAGCGGGGAGTGTCTCACTGTGTGTCAGCGCGCTGATCCGAGCCAGGAGCTGG 154
QY 357 GAGATGAAAAATACAGATTGTTACACAATGCTCGAATGTTGGTGAHAATTCGGGCAAGAC 416
Db 155 GCGACGAGAAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGTGTGGAGAAACCGCACGCGGC 214
QY 417 AAATGGAGTTTACACTCAGAGTGTTCCTCAAGATC----- 449
Db 215 AGGTGGACAGCCACGTTGGAGCTGTTTCGAGCGCAGCAGGAGCTGGGCGACACAGTGGGCA 274
QY 450 -CTGCTGAAAGTGAAACGAGCCTCAGATAAAGAAAGATGATTCACGCCAACAGAAAAGA 508
Db 275 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATCGGTAGCGCAGTCTTGACAAGC 334
QY 509 TCTTCAAGAA--GACCCCGCAGCAGCGGACCAAGTGAAGCCGTGATTTATGTACATGG 566
Db 335 CCAACAGCAAGCGCTCACGGCGCAGCGCAACACGAGAACCGGTGAGAACGCGTCCAGCA 394
QY 567 CAAATGGGATTGAAGACTGTGATGATCAGCCACTAAAGAAAAAATCCAAAGTCAGCAA 626
Db 395 ACCACGACCAGCAGCAGCGGCTCGGGCACACCCAGAGAGAAAGGCCAAGACCTCCA 454
QY 627 AGAAAAAGAAACGCTCCAAAGGCCAAGCAGGAAAGGAAAGCTTCACCTGTTGAGTTTGC 686
Db 455 AGAAGAAGAAAGCGCTCCAAAGGCCAAGCGGAGGAGGCGTCCCTGCGGACCTCCCCA 514
QY 687 TAGATCCTAATGAACCTACATCTGTTATGCAACCAAGTGTCTTATGGGAGATGATAG 746
Db 515 TCGACCCCAACGAAACCCAGTACTGTCTGTGCAACCAAGGTCTCTATGGGGAGATGATCG 574
QY 747 GATGTGACAAATGAACAGTGTCCAATGTAATGTTTCACTTTTTCATGTTTCACTTACCT 806
Db 575 GCTGCGACAAACGACGAGTGCCCAAGTGTGAGTGTTCACCTTCTCGTGGGGGCTCAATC 634
QY 807 ATAAACCAAGGGGAAATGTTATTTGCCAAAGTGCAGGGGAGAGATAATGAGAAAAACAATGG 866
Db 635 ATAAACCAAGGGCAAGTGTACTGTCTCCCAAGTGTCCCGGGGAGAGACGAGAACCATGG 694
QY 867 ACAAAGTACTGAAAGACAAAAAGGATAG 897
Db 695 ACAAGCCCTGGAGAAATCCAAAAAGAGAG 725

RESULT 10

US-09-258-372-1
; Sequence 1, Application US/09258372
; Patent No. 6238918
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,372
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230

FILING DATE: 17.0%; Score 183.8; DB 3; Length 1902;
Query Match
Best Local Similarity 57.0%; Pred. No. 2.2e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;
US-09-258-372-1

ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 109..741

US-09-258-371-9

Sequence 9, Application US/09258371
Patent No. 5986078
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258.371
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900

US-09-258-371-9

Query Match 17.0%; Score 183.8; DB 2; Length 2061;
Best Local Similarity 57.0%; Pred. No. 2.3e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;
US-09-258-371-9

237 AAGAAACGTTAAAGGAAATTTGATGTTTACGAAATAATATAAGAAAGAGATGATTTAA 296
194 AACAGATCTCTGAAGGAGCTAGACGAGTGTCTACGCGCTTCAGTCGCGAGACAGACGGG 253
297 ACCAGAGAAACGTTCTACGAGAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGATTCG 356
254 CGCAGAAAGCGCGGATGCTGCACTGTGTGCGCGCGCTGATCCGACGCCAGGAGCTGG 313
357 GAGATGAAATAATACAGATTGTTACAAATGCTCGAATTTGGTGGAAATTCGGGCAAGAC 416
314 GCGAGAGAGATCCAGATCGTGTAGCCAGATGTTGGAGCTGTGGAGAACCGCACCGGG 373
417 AAATGGAGTTACACTCACAGTGTTCCTCAAGATC----- 449
374 AGTGGACAGCCACCTGGAGCTGTTTCGAGCGCGAGCGAGCTGGCGGACACAGTGGGCA 433
450 -CTGCTGAAGTGAACGAGCCCTCAGATAAGCAAGATGATTCAGCCCAACAGAAAGA 508
434 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGGATCGGTAGCGAGTCTTGAAGC 493
509 TCTTCAAGAA--GACCCCGCAGCGGACCGACCGATGATTTATGTATGTACATGG 566

US-09-258-371-9

Sequence 9, Application US/09258371
Patent No. 5986078
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258.371
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900

US-09-258-371-9

Query Match 17.0%; Score 183.8; DB 3; Length 1902;
Query Match
Best Local Similarity 57.0%; Pred. No. 2.2e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;
US-09-258-372-1

ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 109..741

US-09-258-371-9

Sequence 9, Application US/09258371
Patent No. 5986078
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258.371
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900

US-09-258-371-9

Query Match 17.0%; Score 183.8; DB 2; Length 2061;
Best Local Similarity 57.0%; Pred. No. 2.3e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;
US-09-258-371-9

237 AAGAAACGTTAAAGGAAATTTGATGTTTACGAAATAATATAAGAAAGAGATGATTTAA 296
194 AACAGATCTCTGAAGGAGCTAGACGAGTGTCTACGCGCTTCAGTCGCGAGACAGACGGG 253
297 ACCAGAGAAACGTTCTACGAGAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGATTCG 356
254 CGCAGAAAGCGCGGATGCTGCACTGTGTGCGCGCGCTGATCCGACGCCAGGAGCTGG 313
357 GAGATGAAATAATACAGATTGTTACAAATGCTCGAATTTGGTGGAAATTCGGGCAAGAC 416
314 GCGAGAGAGATCCAGATCGTGTAGCCAGATGTTGGAGCTGTGGAGAACCGCACCGGG 373
417 AAATGGAGTTACACTCACAGTGTTCCTCAAGATC----- 449
374 AGTGGACAGCCACCTGGAGCTGTTTCGAGCGCGAGCGAGCTGGCGGACACAGTGGGCA 433
450 -CTGCTGAAGTGAACGAGCCCTCAGATAAGCAAGATGATTCAGCCCAACAGAAAGA 508
434 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGGATCGGTAGCGAGTCTTGAAGC 493
509 TCTTCAAGAA--GACCCCGCAGCGGACCGACCGATGATTTATGTATGTACATGG 566

Db 494 CCAACAGAGCGCTCACGGCGGCGCAACGAGAACCGTGAGAACGGCTCCAGCA 553
QY 567 CAAATGGGATTAAGACTGTGATGATCAGCCACCTAAAGAAAGAAATCAAGTCAGCAA 626
Db 554 ACCACAGACAGGAGCGGCTCGGGCACACCCAGAGAGAGAGGCGAGACCTCCA 613
QY 627 AGAAAGAAAGCGCTCAAGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 686
Db 614 AGAAGAGAGAGCGCTCAAGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 673
QY 687 TAGATCCTAATGAACCTACATCTGTTATGCAACCAAGTGTCTTATGSGGAGATAG 746
Db 674 TGACCCCAAGCAACCCAGTGTCTGTGCAACCAAGTGTCTTATGSGGAGATAGCG 733
QY 747 GATGTGACATGAACAGTGTCCAAATGAATGGTTTTCATCTTTCATCTTTCATCTTACCT 806
Db 734 GCTGCGACAGAGAGTGTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCG 793
QY 807 ATAAACCAAGGGGAAATGGTATGTCCTCAAGTGTGCAAGGAGGAGGAGGAGGAGGAG 866
Db 794 ATAAACCAAGGCAAGTGTGTCTGTGCAACCAAGTGTGCAACCAAGTGTGCAACCAAG 853
QY 867 ACAGAGTGTGAGAGCAACAAAGAGATAG 897
Db 854 ACAAGCCCTGGAGAAATCCAAAAGAGAG 884

RESULT 12
US-08-751-230-9
; Sequence 9, Application US/08751230
; Patent No. 6117633
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,230
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

; LOCATION: 16..900
US-08-751-230-9
Query Match 17.0%; Score 183.8; DB 3; Length 2061;
Best Local Similarity 57.0%; Pred. No. 2.3e-267;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;
QY 237 AAGAAACGTTAAAGGAAATTTGATGTCTAGCAAAATATATAGAAAGAGATGATTTAA 296
Db 194 AACAGATCTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCGCGAGACACGGGG 253
QY 297 ACCAGAGAAACGCTTACAGCAGCTTCTCCAGAGAGCAGTAAATTAATAGTCAAGAAATGG 356
Db 254 CGCAGAAAGCGGGGATGCTGTGCTGTGTCAGCGCGCTGATCCGAGCAGAGAGTGG 313
QY 357 GAGATGAAAAATACAGATTTGTACACAAATGCTCGAAATTTGGTGGAAATTCGGGCAAGAC 416
Db 314 GCGACGAGAGATTCAGATCGTGAGCCAGATGGTGGAGTGTGGTGGAGAACCCGACGCGGC 373
QY 417 AAATGGAGTTTACACTCACAGTGTTCCTCAAGATC----- 449
Db 374 AGGTGACAGACCGCTGGAGCTGTTTCAGCGCGCAGCAGGAGCTGGGCGACACAGTGGCA 433
QY 450 -CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAGATGATTCAGGCCAACCCAGAAAGA 508
Db 434 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC 493
QY 509 TCTTCAGAA--GACCCCGCAGCGAGCAGTGAAGCCGCTGATTTATGTACATGG 566
Db 494 CCAACAGCAAGCGCTCACGGCGGAGCGCAACAGAGAACCGTGAAGACGCGTCCAGCA 553
QY 567 CAAATGGGATTTGAAGACTGTGATGATCAGCCACTAAAGAAAGAAATCCAACTCAGCAA 626
Db 554 ACCACGACCAAGCAGCGCGCTCGGGCACACCCAGAGAGAGAGGCGCAACACCTCCA 613
QY 627 AGAAAAAGAAACGCTTCAAGGCCAAGCAGAGAAAGGAAAGCTTCACTGTGTAGTTTGC 686
Db 614 AGAAGAGAAAGCGCTTCAAGGCCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 673
QY 687 TAGATCCTAATGAACCTACATCTGTTATGCAACCAAGTGTCTTATGSGGAGATAGTAG 746
Db 674 TCGACCCCAAGCAACCCAGTGTCTGTGCAACCAAGTGTCTTATGSGGAGATAGTAG 733
QY 747 GATGTGACATGAACAGTGTCCAAATGAATGGTTTTCATCTTTCATCTTTCATCTTACCT 806
Db 734 GCTGCGACAAACGAGAGTGTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCG 793
QY 807 ATAAACCAAGGGGAAATGGTATGTCCTCAAGTGTGCAAGGAGGAGGAGGAGGAGGAGGAG 866
Db 794 ATAAACCAAGGCAAGTGTGTCTGTGCAACCAAGTGTGCAACCAAGTGTGCAACCAAG 853
QY 867 ACAGAGTGTGAGAGCAACAAAGAGATAG 897
Db 854 ACAAGCCCTGGAGAAATCCAAAAGAGAG 884
RESULT 13
US-09-499-082-9
; Sequence 9, Application US/09499082
; Patent No. 6143522
; GENERAL INFORMATION:
; APPLICANT: Helbing, Caren C.
; APPLICANT: Riabowol, Karl
; APPLICANT: Johnston, Randall N.
; APPLICANT: Garkavtsev, Igor
; TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA

```

; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/499,082
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,158
; FILING DATE: 27-MAR-1997
; APPLICATION NUMBER: US/08/751230
; FILING DATE: 15-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-854-7400
; TELEFAX: 650-854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..900
; US-09-499-082-9

Query Match 17.0%; Score 183.8; DB 3; Length 2061;
Best Local Similarity 57.0%; Pred. No. 2.3e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;

QY 237 AAGAAAGCTTAAAGGAAATGATGCTTACGAAATAATAAGAAAGAGATGATTAA 296
DB 194 AACAGATCTGAAGGAGTAGAGAGTGCTACAGCGCTTCAGTCGCGACAGACGGGG 253
QY 297 ACCAGAAGAAACGCTTACAGCAGCTTCTCCAGAGAGCCTAAATTAATAGTCAAGAAATGG 356
DB 254 CGCAGAAGCGCGGATGCTGCTGCTGCGAGCGCGCTGATCCGCGAGCAGGAGCTGG 313
QY 357 GAGATGAAATAATACAGATGTTACACAAATGCTCGAATGTTGGTGGAAATTCGGGCAAGAC 416
DB 314 GCAGCAGAGAAGATCCAGATCGTAGCCAGATGTTGGAGCTGTTGGAGAACCGCACCGCGC 373
QY 417 AATGGAGTTTACACTACAGTGTTTCCAAGATC----- 449
DB 374 AGTGGACACCCACGTGGAGCTGTTGAGCGCGAGAGGAGCTGGGCGGACAGTGGGCA 433
QY 450 -CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAGATGGAATTCAGCCCAACAGAAAGA 508
DB 434 ACAGCGCAAGTTGGCGCGACAGGCCCAATGCGATGCGGTAGCGAGCTGTGACAAGC 493
QY 509 TCTTCAAGAA--GACCCCGCAGCGAGCGGACCAAGTGAACCGTGTATTTATGTCATGG 566
DB 494 CCAACAGCAAGCGCTCAGCGCGCGAGCGCAACACGAGAACCGGTGAGAACCGGTCCAGCA 553
QY 567 CAATGGAGTTGAAGACTGTGATGATCAGCCACTTAAAGAAAGAAATCCAACTCAGCAA 626
DB 554 ACCACGACACGAGCGCGCTCGGGGACACCCAGAGAGAAAGAGCGGCAAGCTTCCA 613
QY 627 AGAAAGAAACGCTCCAAAGCCCAAGCAGGAAAGGAGAGCTTCACTCTGTTGAGTTGCA 686
DB 614 AGAAGAAGAGCGCTCCAAAGGCCCAAGCGCGAGAGAGGCGTCCCTCGCGGACCTCCCA 673

; 687 TAGATCCTAATGAACCTACATATCTTATGCAACCAAGTCTTATGGGAGATAG 746
; 674 TCGACCCCAACGAAACCCAGTACTCTCTGTCACCAAGGTCTCTTATGGGAGATAG 733
; 747 GATGTGACAAATGAACAGTGTCCAATGAATGTTTCACTTTTCACTGTGTTCACCTTACCT 806
; 734 GCTGCGACAAACGACGAGTGCCTCCATCGAGTGGTTCCTCTCTGTCGCGGCTCAATC 793
; 807 ATAAACCAAGGGGAATGTTATCCCAAGTGCAGGGGAGATATAGAGAAACAATGG 866
; 794 ATAAACCAAGGGCAAGTGTACTGTCCCAAGTGCAGGGGAGAACGAGAACCATGG 853
; 867 ACAAAGTACTGAAAAGAGCAAAAAAGGATAG 897
; 854 ACAAAGCCTTGAGAAATCCAAAAAGAGAG 884

RESULT 14
US-09-258-372-9
; Sequence 9, Application US/09258372
; Patent No. 6238918
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,372
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
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; LOCATION: 16..900
; US-09-258-372-9

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QY 237 AAGAAAGCTTAAAGGAAATGATGCTTACGAAATAATAAGAAAGAGATGATTAA 296
DB 194 AACAGATCTGAAGGAGTAGAGAGTGCTACAGCGCTTCAGTCGCGACAGACGGGG 253

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297 ACCAGAGAAACGCTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAAATGG 356
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314 GCGACGAGAAGATCCAGATCTGTAGCCAGATGTGGAGCTGTGGAGAAACCGCACGGGC 373
417 AAATGGAGTTACACTCACAGTGTGTTCGAAGATC----- 449
374 AGGTGACACACGACGCTGGAGCTGTTCTGAGCGCAGCAGGAGCTGGCGCACAGTGGCA 433
450 -CTGCTGAAAGTGAACAGCGCTCAGATAAAGCAAGATGATTCAGCCCAACAGAAAGA 508
434 ACAGCGGCAAGTGTGGCGGACAGCCCAATGGCGATCGGTAGCGCAGTCTGTCAAGC 493
509 TCTTCAAGAA--GACCCCGCAGCGCAGCGGACAGTCAAGCCGCTGATTTATGTCAATGG 566
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567 CAAATGGGATTGAAGACTGTGATGATCAGCCACTTAAAGAAAGAAATCCAAAGTCAGCAA 626
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RESULT 15

US-09-006-783A-2
; Sequence 2, Application US/09006783A
; Patent No. 6297366
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrey V
; APPLICANT: Garkavstev, Igor
; APPLICANT: Rabinowol, Kari
; TITLE OF INVENTION: p33/INGI as a Mediator of p53 Signaling
; TITLE OF INVENTION: Pathway
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,783A
; FILING DATE: 15-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

Search completed: January 12, 2004, 17:23:53
Job time : 99 secs

NAME: No. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 2061 base pairs
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TOPOLOGY: linear
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FEATURE:
NAME/KEY: CDS
LOCATION: 16..897
US-09-006-783A-2

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DB 854 ACAAGCCCTGGAGAAATCCAAAAAGAGAG 884

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3
Konno, H., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Shibata, K., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
Sumi, N., Ighii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system -384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
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Quackenbush, J., Schraml, L.M., Staubli, F., Suzuki, R., Tomita, M.,
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Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
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Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.,
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
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21085660
11217851

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AUTHORS

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The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

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6 (bases 1 to 2643)
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Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tonaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

TITLE
JOURNAL

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

FEATURES

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ORGANISM	Homo sapiens		
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AUTHORS	NIH-MGC http://imgc.nci.nih.gov/		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: NCI cDNA Library Preparation: Michael Brownstein Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2058 row: h column: 10 High quality sequence stop: 587.		
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AUTHORS 1 (bases 1 to 793)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
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the laboratory of Gerald M. Rubin (University of
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1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

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/clone="IMAGE:3941655"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."


```

MEDLINE      21227151
PUBMED       11329013
COMMENT      Contact: Scott J. Cain
              Athersys, Inc.
              3201 Carnegie Ave, Cleveland, OH 44115, USA
              Tel: 216 431 9900
              Fax: 216 361 9596
              Email: scain@atersys.com
              High quality sequence stop: 439.
              Location/Qualifiers
                1. 919
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone_lib="HT1080"
                /notes="See 'Athersys RAGE Library'
                /notes="See 'Creation of Genome-wide Protein Expression
                Libraries using Random Activation of Gene Expression',
                Nature Biotechnology, in press. Note that even though the
                cell type indicated is HT1080, since a random activation
                method was used, these sequence tags are not necessarily
                expressed in HT1080 under normal circumstances."
BASE COUNT   332 a 151 c 216 g 216 t 4 others
ORIGIN
Query Match  63.0%; Score 680.8; DB 10; Length 919;
Best Local Similarity 95.1%; Pred. No. 4.9e-76;
Matches 788; Conservative 0; Mismatches 30; Indels 11; Gaps 8;

QY 236 CAAAGAACGTTAAAGCAAAATGTATGATGCTCAGCAAAAATATAGAAAGAGATGATTAA 295
DB 1 CCAAGAACGTTAAAGCAAAATGTATGATGCTCAGCAAAAATATAGAAAGAGATGATTAA 60

QY 296 AACCAGAAGAAACGCTCTACAGAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAAATTG 355
DB 61 AACCAGAAGAAACGCTCTACAGAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAAATTG 120

QY 356 GGAGATGAAATAATACAGATTGTTACACAATCTCGAATGCTGGAATCGGCAAGA 415
DB 121 GGAGATGAAATAATACAGATTGTTACACAATCTCGAATGCTGGAATCGGCAAGA 180

QY 416 CAAATGGAGTTACACTCACAGTGTCTTCCAGAGTCTCTGCTGAAAGTGAACGAGCTCAGAT 475
DB 181 CAAATGGAGTTACACTCACAGTGTCTTCCAGAGTCTCTGCTGAAAGTGAACGAGCTCAGAT 240

QY 476 AAAGCAAGATGATTTCCAGCCCAACCAAGAAAGATCTTCAAGAAAGACCCCGCAGCGCG 535
DB 241 AAAGCAAGATGATTTCCAGCCCAACCAAGAAAGATCTTCAAGAAAGACCCCGCAGCGCG 300

QY 536 ACCAGTGAAGCCGCTGATTTATGTCATCGGCAATGGGATTTGAAGACTGTGATGATCAG 595
DB 301 ACCAGTGAAGCCGCTGATTTATGTCATCGGCAATGGGATTTGAAGACTGTGATGATCAG 360

QY 596 CCACCTTAAGAAAGAAATCCAAAGTCAAGCAAGAAAGAAAGCGCTTCAAGGCGCAAGCAG 655
DB 361 CCACCTTAAGAAAGAAATCCAAAGTCAAGCAAGAAAGAAAGCGCTTCAAGGCGCAAGCAG 420

QY 656 GAAAGGGAAGCTTCACTGTTGATGTTTGCATATAGATCTTAATGAACCTACATCTGCTTA 715
DB 421 GAAAGGGAAGCTTCACTGTTGATGTTTGCATATAGATCTTAATGAACCTACATCTGCTTA 480

QY 716 TGAACCAAGTGTCTTATGGGGAGATGATAGATGTGACATGAACAGTGTCCAATTGAA 775
DB 481 TGAACCAAGTGTCTTATGGGGAGATGATAGATGTGACATGAACAGTGTCCAATTGAA 540

QY 776 TGGTTTCACTTTTCATGTTTTCACCTTACCTATAACCAAGGGAAGTGGTATTCGCCA 835
DB 541 TGGTTTCACTTTTCATGTTTTCACCTTACCTATAACCAAGGGAAGTGGTATTCGCCA 600

QY 836 AAGTCAGGGGAGATTAATGAGAAACAAATGGACAAAGTACTGAAAGACCAAAAAAGGAT 895
DB 601 AAGTCAGGGGAGATTAATGAGAAACAAAGTACTGAAAGACCAAAAAAGG-T 657

```

```

QY 896 AGAAGATCAGGTAGTAAAGGCCATCCACATTTAAAGGGTATTATGCTTTTATATAAT 955
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QY 956 TCGTTTCTTTTCAGAAAATGTTTATAGGTAATGATGATGATGATGATGATGATGATGAT 1015
DB 715 TCGATTGCTTTTAAAAAATG-TTATAGGTAATGTC-TTATAGGTAATGTC-TTATNTAAT 770

QY 1016 CATTAGTATTAAATGTTGTTATTAATAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1064
DB 771 CATTAGTATTAAATG-GGATAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818

RESULT 10
LOCUS      BM682789/c
DEFINITION UI-E-EJ1-ajf-g-22-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone
ACCESSION BM682789
VERSION    BM682789.1 GI:18992685
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 675)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE      Normalization and subtraction: two approaches to facilitate gene
JOURNAL    Genome Res. 6 (9), 791-806 (1996)
MEDLINE    97044477
PUBMED     8889548
COMMENT    Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Forward
            POLYA=Yes.

FEATURES             Location/Qualifiers
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     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone_lib="UI-E-EJ1"
     /tissue_type="fetal eyes, lens, eye anterior segment,
     optic nerve, retina, Retina Foveal and Macular, RPE and
     Choroid"
     /dev_stage="fetal and adult"
     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
     /clone_lib="UI-E-EJ1"
     /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
     modified polylinker; Site 1: EcoR I; Site 2: Not I;
     UI-E-EJ1 is a subtracted cDNA library constructed
     according to Bonaldo, Lennon and Soares, Genome Research,
     6:791-806, 1996. First strand cDNA synthesis was primed
     with an oligo-dT primer containing a Not I site. Double
     stranded cDNA was ligated to an EcoR I adaptor, digested
     with Not I, and cloned directionally into pT73-Pac
     vector. The oligonucleotide used to prime the synthesis of
     first-strand cDNA contains a library tag sequence that is
     located between the Not I site and the (dT)18 tail. The
     sequence tags for this library are: fetal eyes, AGAATCAAGA
     ; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT;
     optic nerve, CCATTAAAGTG; retina, CCGCG; Retina Foveal and

```

Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG LIB=UI-E-EJ1
TAG TISSUE=Retina and Macular Retina
TAG_SEQ=GTCC

BASE COUNT 164 a 148 c 110 g 253 t
ORIGIN

Query Match 62.2%; Score 671.8; DB 12; Length 675;
Best Local Similarity 99.7%; Pred. No. 7.8e-75;
Matches 673; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 398 GTGGAATCGGCAAGACAAATGGATTACACTCAGTGTTCCTCAAGATCCTGCTGAA 457
DB 675 GTGGAATCGGCAAGACAAATGGATTACACTCAGTGTTCCTCAAGATCCTGCTGAA 616
QY 458 AGTGAACGACCTCAGATAAGCAAGATGGATTCGACCAACAGAAAGATCTCAAGA 517
DB 615 AGTGAACGACCTCAGATAAGCAAGATGGATTCGACCAACAGAAAGATCTCAAGA 556
QY 518 AGACCCCGCAGGCGGACGAGTGAAGCCGATTTATGTACATGGCAATGGGATT 577
DB 555 AGACCCCGCAGGCGGACGAGTGAAGCCGATTTATGTACATGGCAATGGGATT 496
QY 578 GAAGACTGTGATGATCAGCCACCTAAAGAAAGAAATCCAAGTCAGCAAGAAAGAAA 637
DB 495 GAAGACTGTGATGATCAGCCACCTAAAGAAAGAAATCCAAGTCAGCAAGAAAGAAA 436
QY 638 CGTCCAGGCCAAGCAAGAAAGGAGCTTCACTGTTGAGTTGCAATAGATCTTAAT 697
DB 435 CGTCCAGGCCAAGCAAGAAAGGAGCTTCACTGTTGAGTTGCAATAGATCTTAAT 376
QY 698 GRACCTACATCTGCTTATGCAACCAAGTCTTATGGGAGATGATAGATGTGCAAT 757
DB 375 GRACCTACATCTGCTTATGCAACCAAGTCTTATGGGAGATGATAGATGTGCAAT 316
QY 758 GAACAGTGTCCAATGGAATGGTTTCACTTTCATGTGTTTCACTTACCTATAACCAAG 817
DB 315 GAACAGTGTCCAATGGAATGGTTTCACTTTCATGTGTTTCACTTACCTATAACCAAG 256
QY 818 GGAATATGTTATGCCCCAAGTCAGGGAGATAATGAGAAACAAATGGACAAAGTACT 877
DB 255 GGAATATGTTATGCCCCAAGTCAGGGAGATAATGAGAAACAAATGGACAAAGTACT 196
QY 878 GAAAGACAAAGAGATAGAGATCGAGTAGTAAGGCTCCATTTTAAAGGTT 937
DB 195 GAAAGACAAAGAGATAGAGATCGAGTAGTAAGGCTCCATTTTAAAGGTT 136
QY 938 ATTGTCTTTATATATCTGTTTCTTCCAGAAATGTTTATAGGTAATGATTAAGAC 997
DB 135 ATTGTCTTTATATATCTGTTTCTTCCAGAAATGTTTATAGGTAATGATTAAGAC 76
QY 998 TATGCAATATTTTATATCTGTTTATATGTTTATTAAGATTTGTTTACTTTGAA 1057
DB 75 TATGCAATATTTTATATCTGTTTATATGTTTATTAAGATTTGTTTACTTTGAA 16
QY 1058 AAAAAAAAAAAAAA 1072
DB 15 AAAAAAAAAAAAAA 1

RESULT 11
BM719460
LOCUS
DEFINITION
UI-E-EJ1-af-f-g-22-0-UI.r1 UI-E-EJ1 Homo sapiens cdna clone
UI-E-EJ1-af-f-g-22-0-UI 5', mRNA sequence.
BM719460
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 664)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.regen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
I. .664
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-af-f-g-22-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
/note="Organ: eye; Vector: p7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT;
optic nerve, CCATTAAAGT; retina, CCGCG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."

FEATURES
source

BASE COUNT 241 a 111 c 149 g 162 t
ORIGIN

Query Match 61.4%; Score 663; DB 12; Length 664;
Best Local Similarity 99.8%; Pred. No. 9.8e-74;
Matches 663; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 377 GTTACACAAATGCTCGAATTTGGTGGAAATCGGGCAAGACAAATGGAGTTACACTCACAG 436
DB 1 GTTACACAAATGCTCGAATTTGGTGGAAATCGGGCAAGACAAATGGAGTTACACTCACAG 60
QY 437 TGTTCACAGATCTCTGAAAGTGAACGAGCTCAGATAAGCAAGATGGATTCCAGC 496
DB 61 TGTTCACAGATCTCTGAAAGTGAACGAGCTCAGATAAGCAAGATGGATTCCAGC 120
QY 497 CAACAGAAAGATCTTCAAGAGAGACCCCGCAGCGACGACGACGAGTGAAGCCGTGATTTA 556
DB 121 CAACAGAAAGATCTTCAAGAGAGACCCCGCAGCGACGACGAGTGAAGCCGTGATTTA 180
QY 557 TGTTCACATGGCAATGGGATTTGAAGACTGTGTGATGATCAGCCACCTAAAGAAAGAAATCC 616
DB 181 TGTTCACATGGCAATGGGATTTGAAGACTGTGTGATGATCAGCCACCTAAAGAAAGAAATCC 240

QY 617 AGTCTCAGCAAGAAAAAGAAACGCTCAAGGCCAAGCAGGAAAGGAAAGGAGCTTCCACCTGTT 676
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 Db 241 AGTCTCAGCAAGAAAAAGAAACGCTCAAGGCCAAGCAGGAAAGGAAAGGAGCTTCCACCTGTT 300
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 QY 677 GAGTTTGCATAGATCCTAATGAACCTACATACCTGCTTATGCAACCAAGTGTCTTATGGG 736
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 Db 301 GAGTTTGCATAGATCCTAATGAACCTACATACCTGCTTATGCAACCAAGTGTCTTATGGG 360
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 QY 737 GAGATGATGAGTGTGACAAATGAACAGTGTCCAAATGAATGATGTTTCACTTTTCATGTTT 796
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 Db 361 GAGATGATGAGTGTGACAAATGAACAGTGTCCAAATGAATGATGTTTCACTTTTCATGTTT 420
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 QY 797 TCACCTTACCTATATAACCAAGGGGAAATGTTATGCCCCAAAGTGACGGGAGAGATAATGAG 856
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 Db 421 TCACCTTACCTATATAACCAAGGGGAAATGTTATGCCCCAAAGTGACGGGAGAGATAATGAG 480
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 QY 857 AAAACAATGACAAAAAGTACTGAAAAAGACAAAAAAGGATAGAAAGTCGAGGTAGTAAAGG 916
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 Db 481 AAAACAATGACAAAAAGTACTGAAAAAGACAAAAAAGGATAGAAAGTCGAGGTAGTAAAGG 540
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 QY 917 CCATCCACATTTTAAAGGGTTATTTGCTTTTATATAATTCGTTTTCGTTTTCAGAAAATGT 976
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 Db 541 CCATCCACATTTTAAAGGGTTATTTGCTTTTATATAATTCGTTTTCGTTTTCAGAAAATGT 600
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 QY 977 TTTAGGGTAAATGCATAAGACTATGCAATAATTTTAAATCATTAGTATTAAATGCTGTATT 1036
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 Db 601 TTTAGGGTAAATGCATAAGACTATGCAATAATTTTAAATCATTAGTATTAAATGCTGTATT 660
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 QY 1037 AAAA 1040
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 Db 661 AAAA 664

RESULT 12
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 HOMO sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Roberton,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R.
 and Morton,C.C.
 Isolation of novel and known genes from a human fetal cochlear cDNA
 library using subtractive hybridization and differential screening
 Genomics 23, 42-50 (1994)
 95130111
 7829101
 Contact: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).
 This clone is available royalty-free through LILNI; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plats: LLAM327 row: G column: 7
 Seq primer: 17 primer.
 Location/Qualifiers
 1. .653
 /organism="Homo sapiens"
 /mol_type="mRNA"

FEATURES

source

RESULT 13
 BI091047/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS

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 602855235F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996593 5',
 mRNA sequence.
 BI091047
 BI091047.1 GI:14509377
 EST.

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 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dT. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

BASE COUNT 160 a 146 c 106 g 241 t

Query Match 58.9%; Score 636.4; DB 12; Length 653;
 Best Local Similarity 99.8%; Pred. No. 2.1e-70;
 Matches 637; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 435 AGTGTTCACAGATCCTGCTGAAGTGAACGAGCCTCAGATAAGCAGAGATGGATTCCA 494
 |||||
 Db 653 AGTGTTCACAGATCCTGCTGAAGTGAACGAGCCTCAGATAAGCAGAGATGGATTCCA 594
 |||||
 QY 495 GCCAACCCAGAAAGATCTTCAAGAACACCCCGCAGGCGGACCGACAGTGAAGCCGTGATT 554
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 Db 593 GCCAACCCAGAAAGATCTTCAAGAACACCCCGCAGGCGGACCGACAGTGAAGCCGTGATT 534
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 QY 555 TATGTCAATGTCGCAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAAT 614
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 QY 615 CCAAGTCAGCAAGAAAGAAAGAACGCTCCAAAGCCAGCAGGAAAGGGAGCTTCCACCTG 674
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 Db 473 CCAAGTCAGCAAGAAAGAAAGAACGCTCCAAAGCCAGCAGGAAAGGGAGCTTCCACCTG 414
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 Db 413 TTGAGTTTGCATAGATCCTAATGAACCTACATCTGCTTATGCAACCAAGTGTCTTATG 354
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 Db 353 GGGAGATGATAGGATGTGACAAATGAACAGTGTCCAAATGGAATGGTTTTCATGTTG 294
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 Db 293 TTTCTCTTACCTATAAACCAGAGGGGAATGTTGCCCAAGTCCAGGGAGAGATAATG 234
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 Db 233 AGAAAACAATGACAAAAGTACTGAAAAGACAAAAGAGATAGAAGATCGAGGTAGTAAA 174
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 QY 915 GGCCATCCACATTTTAAAGGGTTATTTGCTTTTATATAATTCGTTTTCAGAAAAT 974
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 QY 1035 TTAAGAGTTGTGTACTTTGAAAAAAGAAAAAAGAAAAA 1072
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 Db 53 TTAAGAGTTGTGTACTTTTAAAAAAGAAAAAAGAAAAA 16
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 891)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM1022 row: e column: 10
High quality sequence stop: 722.
Location/Qualifiers
1. .891
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:4996593"
/cell_line="MGC36"
/lab_host="DH10B"
/clone_lib="NIH_MGC_10"
/notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5 kb. Library prepared by Life Technologies."
BASE COUNT 237 a 199 c 149 g 306 t
ORIGIN
Query Match 58.5%; Score 632.2; DB 12; Length 891;
Best Local Similarity 96.5%; Pred. No. 5.8e-70;
Matches 687; Conservative 0; Mismatches 21; Indels 4; Gaps 4;
QY 336 TAATTAATAGTCAAGATTCGGAGATGAAATACAGA-TTGTACACAAATGCTCGAA 394
Db 711 TAATTAATAGTCAAGATTCGGAGATGATTTATATACAGATTGACACTAAATGCTCGAA 652
QY 395 TTGGTGAATCGGCAAGACAAATGGAGTTACACTCACAGTGTTCACAGATCTGT-C 453
Db 651 TTGGTGTATATC-GGCAAGACATATGGAGTTACACTCACAGTGTTCACAGATCTGT-C 593
QY 454 TGAAGTGAACGAGCTTCAGATAAGCAAGAT-GGATTCAGCCCAACCAAGAGATCTT 512
Db 592 TGAAGTGAACGAGCTTCAGATAAGCAAGATGGGATTCAGCCCAACCAAGAGATCTT 533
QY 513 CAAGAGACCCCGCAGCGGACGAGTGAAGCCGTGATTTATGTCACATGGCAATG 572
Db 532 CAAGAGACCCCGCAGCGGACGAGTGAAGCCGTGATTTATGTCACATGGCAATG 473
QY 573 GGAATTGAAGTGTGATGATCAGCCACTTAAAGAAAGAAATCAAGTCAAGCAAGAA 632
Db 472 GGAATTGAAGTGTGATGATCAGCCACTTAAAGAAAGAAATCAAGTCAAGCAAGAA 413
QY 633 AGAAACGCTCAAGGCGCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCATAGATC 692
Db 412 AGAAACGCTCAAGGCGCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCATAGATC 353
QY 693 CTAATGACCTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAGGATGTG 752
Db 352 CTAATGACCTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAGGATGTG 293
QY 753 ACAATGAACAGTGTCCAAATTTGAATGTTTTCATTTTCATGTTTTCATTTACCTATAAC 812
Db 292 ACACTGAACAGTGTCCAAATTTGAATGTTTTCATTTTCATGTTTTCATTTACCTATAAC 233
QY 813 CAAAGGGGAATGGTATTTGCCAAAGTGCAGGGGAGATAATGAGAAACCAATGGAACAAA 872

Db 232 CAAAGGGGAATGGTATTTGCCAAAGTGCAGGGGAGATATGAGAAACCAATGACACAAA 173
QY 873 GTACTGAAAGACAAAAGAGATAGAGATCGAGGTAGTAGTAAGGCCATCCACATTTTAAA 932
Db 172 GTACTGAAAGACAAAAGAGATAGAGATCGAGGTAGTAGTAAGGCCATCCACATTTTAAA 113
QY 933 GGGTTAATTTGCTTTTATATATAATTCGTTGCTTTCAGAAAATGTTTTCAGGTAATGCAT 992
Db 112 GGGTTAATTTGCTTTTATATATAATTCGTTGCTTTCAGAAAATGTTTTCAGGTAATGCAT 53
QY 993 AGACTATGCCATAATTTTATATATAATTCATAGTATTAATGCTGATTAATGAGTTG 1044
Db 52 AGACTATGCCATAATTTTATATATAATTCATAGTATTAATGCTGATTAATGAGTTG 1
RESULT 14
LOCUS BI460319 708 bp mRNA linear EST 21-AUG-2001
DEFINITION G03201967F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5267729 5', mRNA sequence.
ACCESSION BI460319
VERSION BI460319.1 GI:15250975
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 708)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM1675 row: f column: 18
High quality sequence stop: 700.
Location/Qualifiers
1. .708
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:5267729"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/notes="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to 80T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 209 a 163 c 213 g 122 t 1 others
ORIGIN
Query Match 56.2%; Score 607; DB 12; Length 708;
Best Local Similarity 98.9%; Pred. No. 9.2e-67;
Matches 621; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 10 GCGGTGCAATGTCGGCTCTGATCGGAGCGGCGGCGGATCGGAGATCGGAGAT 69
Db 81 GCGGTGCAATGTCGGCTCTGATCGGAGCGGCGGCGGATCGGAGATCGGAGAT 140
QY 70 GTTAGGGCAGCAGCAGCACTGTACTCGTTCGCTCGCTCTCTGACCGGGGAGCGGAG 129

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2004, 16:38:42 ; Search time 334 Seconds
(without alignments)
8728.722 Million cell updates/sec

Title: US-09-513-365A-2
Perfect score: 1080
Sequence: 1 gcggcgccggcggtgcgtg.....aaaaaaaaaaaaaaaaaaaaa 1080

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1080	100.0	1080	22	AAD12783
2	1046	96.9	1078	20	AZ08596
3	838.4	77.6	840	20	AZ08595
4	825.2	76.4	1153	21	AZ47473
5	825.2	76.4	1154	24	ABS70424
6	332.2	30.8	346	21	AAC28459
7	325	30.1	325	21	AZ47474
8	253.6	23.5	2817	21	AAA53790

9	237.4	22.0	911	21	AAA53792	Human P37ING1 codi
10	236	21.9	1533	22	AAH28478	Nucleotide sequenc
11	236	21.9	2897	24	ABK86977	Human inhibitor of
12	197.2	18.3	1835	21	AAH53789	Murine ingl common
13	183.8	17.0	1143	22	AAH28479	Nucleotide sequenc
14	183.8	17.0	1902	18	AAH69651	Tumour suppressor
15	183.8	17.0	1902	19	AAV62285	Partial INGI parti
16	183.8	17.0	2061	18	AAH69652	Tumour suppressor
17	183.8	17.0	2061	19	AAV62292	Human INGI full-le
18	183.4	17.0	8487	22	AAH37089	Human musculoskele
19	183.4	17.0	8487	25	ABX60077	cDNA encoding nove
20	183.4	17.0	163350	24	AAH46127	Human tumour suppr
21	183	16.9	1905	24	AAH46126	Human tumour suppr
22	182.4	16.9	2886	24	ABK86976	Human inhibitor of
23	182.2	16.9	2061	20	AAH28688	Nucleotide sequenc
24	175	16.2	825	22	AAH03733	Human cDNA clone (
25	143	13.2	742	22	AAH28480	Nucleotide sequenc
26	142.6	13.2	857	22	AAH28481	Nucleotide sequenc
27	125.8	11.6	693	24	ABQ50058	Oligonucleotide fo
C 28	125.8	11.6	693	24	ABQ50059	Oligonucleotide fo
C 29	124.6	11.5	693	24	ABQ50060	Oligonucleotide fo
30	124.6	11.5	693	24	ABQ50061	Oligonucleotide fo
31	109.2	10.1	1082	25	ABQ77429	Human CGDD cDNA 72
32	102	9.4	108	16	AAH23370	Human gene signatu
33	101.4	9.4	1465	22	AAK52101	Human polynucleoti
34	98.8	9.1	987	23	ABL15055	Drosophila melanog
C 35	97	9.0	693	22	ABA08933	Human IKK binding
36	97	9.0	958	22	AAF90402	Cell cycle protein
37	97	9.0	1108	22	AAF90399	Cell cycle protein
38	97	9.0	1300	24	ABZ11521	Human polynucleoti
39	95.6	8.9	678	21	AAA27423	IkappaB kinase (IK
40	95.6	8.9	699	21	AAA27422	IkappaB kinase (IK
41	91.8	8.5	1856	22	AAI60334	Human polynucleoti
C 42	91.6	8.5	1336	24	ABQ54665	Human ovarian anti
43	91.6	8.5	1807	22	AAH12782	cDNA encoding huma
44	91.6	8.5	1819	25	ABZ23614	Cofactor 33a (CF33
C 45	91.6	8.5	1819	25	ABZ23615	Cofactor 33a (CF33

ALIGNMENTS

RESULT 1
AAD12783
ID AAD12783 standard; DNA; 1080 BP.

AC AAD12783;

DT 23-OCT-2001 (first entry)

DE Tumour suppressor homologue protein, p33ING2 DNA.

XX Tumour suppressor; p47ING3; cell proliferation; cellular aging; p33ING2;
KW anchorage dependence; apoptosis; tumour; cancer; gene therapy; ds.

XX Unidentified.

XX Key Location/Qualifiers
FH CDS 68..910
FT /*tag= a
FT /product= "Tumour suppressor homologue protein, p33ING2"

PN WO200159114-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04425.

XX 09-FEB-2000; 2000US-0181292.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Harris CC, Nagashima M;

CC apoptosis and the pathology of cancer, the diagnosis and treatment of
CC cancer such as cancer of the colon, stomach, oesophagus or fallopian
CC tube, and the screening of candidate drugs for the treatment of such
CC cancers.
XX
SQ Sequence 1078 BP; 356 A; 206 C; 280 G; 236 T; 0 other;

Query Match 96.9%; Score 1046; DB 20; Length 1078;
Best Local Similarity 99.5%; Pred. No. 4.9e-229;
Matches 1049; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
QY 1 GCGGCGCGCGCGTGCATGTCGGCTGCTGGATGCGGAGCGCGCGCGCGCGGAT 60
D 25 GCGGCGCGCGCGCGTGCATGTCGGCTGCTGGATGCGGAGCGCGCGCGCGCGGAT 84
QY 61 GCGCAGGATGTTAGGCGCAGCAGCAGCAACCTGTAATGCTGCGCTCGCTCTGACCGG 120
D 85 GCGCAGGATGTTAGGCGCAGCAGCAGCAGCAACCTGTAATGCTGCGCTCGCTCTGACCGG 144
QY 121 GGAGCGAGCGCGCTGCTACCTGCTACGTCGAGGACTACCTTGGTGGGTCGCT 180
D 145 GGAGCGAGCGCGCTGCTACCTGCTACGTCGAGGACTACCTTGGTGGGTCGCT 204
QY 181 GCGCCACGACATCCAGAGGACGTCGTCGTCGAGAGCTCGACAAACAATATCAAGA 240
D 205 GCGCCACGACATCCAGAGGACGTCGTCGTCGAGAGCTCGACAAACAATATCAAGA 264
QY 241 AAGCTTAAAGAAATGATGATGCTCTACGAAATATAGAAAGAGATGATTTAAACA 300
D 265 AAGCTTAAAGAAATGATGATGCTCTACGAAATATAGAAAGAGATGATTTAAACA 324
QY 301 GAAGAAACGCTACAGCAGCTTCTCCAGAGAGCACTAAATTAATAGTCAAGAAATGGGAGA 360
D 325 GAAGAAACGCTACAGCAGCTTCTCCAGAGAGCACTAAATTAATAGTCAAGAAATGGGAGA 384
QY 361 TGAAGAAATACAGATGTTTACAAATGCTCGAAATGTTGGGAAATCGGCGCAAGACAAAT 420
D 385 TGAAGAAATACAGATGTTTACAAATGCTCGAAATGTTGGGAAATCGGCGCAAGACAAAT 444
QY 421 GGAAGTTACACTACAGTGTTCACAGATCTGCTGAAAGTGAACGAGCCTTCAGATAAGC 480
D 445 GGAAGTTACACTACAGTGTTCACAGATCTGCTGAAAGTGAACGAGCCTTCAGATAAGC 504
QY 481 AAGATGGATTCAGGCAACAGAAAGATCTTCAAGAGAGCCCGCAGGCGGAGCCAG 540
D 505 AAGATGGATTCAGGCAACAGAAAGATCTTCAAGAGAGCCCGCAGGCGGAGCCAG 564
QY 541 TGAAGCCGCTGATTTATGTCATATGGCAATGGATGGAAGTGTGATGATCAGCCACC 600
D 565 TGAAGCCGCTGATTTATGTCATATGGCAATGGATGGAAGTGTGATGATCAGCCACC 624
QY 601 TAAAGAAAGAAATCCAGTCCAGCAAGAAAGAAACGCTCCAAGGCCAGCAGAAAG 660
D 625 TAAAGAAAGAAATCCAGTCCAGCAAGAAAGAAACGCTCCAAGGCCAGCAGAAAG 684
QY 661 GGAAGCTTCACTGTTGAGTTTCAATAGATCTCAATGAACTTACATCTGCTTATGCAA 720
D 685 GGAAGCTTCACTGTTGAGTTTCAATAGATCTCAATGAACTTACATCTGCTTATGCAA 744
QY 721 CCAAGTGTCTTATGGGAGATGATAGATGTGCAATGAACAGTGTCCAATTTGAATGGTT 780
D 745 CCAAGTGTCTTATGGGAGATGATAGATGTGCAATGAACAGTGTCCAATTTGAATGGTT 804
QY 781 TCATTTTCATGTTTCACTTACCTTATAACCAAGGGGAATGTTATTTGCCAAAGTG 840
D 805 TCATTTTCATGTTTCACTTACCTTATAACCAAGGGGAATGTTATTTGCCAAAGTG 864
QY 841 CAGGGAGATTAATGAGAAACAAATGACAAAGTCTGAAAGACAAAGGATAGAG 900
D 865 CAGGGAGATTAATGAGAAACAAATGACAAAGTCTGAAAGACAAAGGATAGAG 924
QY 901 ATCAGGATAGTAAGGCCATCCACATTTTAAAGGGTTATTTGCTTTTATATATTCGTT 960
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Db 925 ATCAGGATAGTAAGGCCATCCACATTTTAAAGGGTTATTTGACTATATATATCCGTT 984
QY 961 TGCTTTTCAGAAAATGTTTTCAGGTAATGCATAAGAGCTATGCAATATTTTATCATTA 1020
D 985 TGCTTTTCAGAAAATGTTTTCAGGTAATGCATAAGAGCTATGCAATATTTTATCATTA 1044
```

```
QY 1021 GTATTAATCGTGTATTTAAAGTGTGTGTACTTTG 1054
D 1045 GTATTAATCGTGTATTTAAAGTGTGTGTACTTTG 1078
```

RESULT 3
AAZ08595

ID AAZ08595 standard; cDNA; 840 BP.

XX AAZ08595;

DT 18-OCT-1999 (first entry)

XX Human ING1L encoding cDNA.

XX Human; TSC403; ING1L; diagnosis; lung cancer; cell cycle; regulation;
cell proliferation; cell aging; apoptosis; tumour suppressor; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..840

FT /tag= a

FT /product= "ING1L"

FT /note= "no stop codon given"

XX WO9940190-A1.

XX 12-AUG-1999.

XX 02-FEB-1999; 99WO-JP00419.

XX 28-APR-1998; 98JP-0134679.

XX 03-FEB-1998; 98JP-0038133.

XX 05-MAR-1998; 98JP-0073234.

XX (SAKA) OTSUKA PHARM CO LTD.

XX Horie M, Nagata M, Ozaki K, Shimada Y;

XX WPI; 1999-494294/41.

XX P-PSDB; AAY29606.

XX Human lung-specific gene TSC430 overexpressed in cancer tissue, used
for treatment of, e.g. colon tumour

XX Claim 14; Page 91; 99pp; Japanese.

XX The present sequence represents the human tumour suppressor gene ING1L.
The present invention also describes the human gene TSC403 expressed
specifically in normal lung tissue. TSC403 is useful in the
diagnosis, investigation and treatment of cancers in which it is
overexpressed, including cancer of the lung, breast, fallopian tube,
oesophagus, colon, thyroid, parotid gland, bladder, ovary or pancreas.
ING1L is useful in the investigation of cell proliferation, aging and
apoptosis and the pathology of cancer, the diagnosis and treatment of
cancer such as cancer of the colon, stomach, oesophagus or fallopian
tube, and the screening of candidate drugs for the treatment of such
cancers.

XX Sequence 840 BP; 297 A; 164 C; 211 G; 168 T; 0 other;

Query Match 77.6%; Score 838.4; DB 20; Length 840;

Best Local Similarity 99.9%; Pred. No. 1.1e-181;

Matches 839; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 68 ATGTTAGGCGCAGCAGCAGCAACTGTACTCGTCGGCTCGCTCTGACCGGGAGCGG 127

Db 720 AAAGAACCGCTCAAGCCCAAGCAGGAAAGGGAGCTTCACCTGTTGAGTTTGCATAGA 779
QY TCCTAATGAACCTACATACCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATGATG 750
Db 780 TCCTAATGAACCTACATACCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATGATG 839
QY 751 TGCAATGAACAGTGTCCCAATGAATGGTTTCACTTTTCATGTTTCACTTACCTATAA 810
Db 840 TGCAATGAACAGTGTCCCAATGAATGGTTTCACTTTTCATGTTTCACTTACCTATAA 899
QY 811 ACCAAGGGGAAATGTTATGCCCCAAGTGCAGGGGAGATTAATGAGAAAACAATGACAA 870
Db 900 ACCAAGGGGAAATGTTATGCCCCAAGTGCAGGGGAGATTAATGAGAAAACAATGACAA 959
QY 871 AAGTACTGAAAAGACAAAAGGATAGAGATCGAGTGTAGTAAGAGGCCATCCACATTTTA 930
Db 960 AAGTACTGAAAAGACAAAAGGATAGAGATCGAGTGTAGTAAGAGGCCATCCACATTTTA 1019
QY 931 AAGGGTTATTGTTCTTTTATATTAATTCGTTTGTCTTTCAGAAAATGTTTATAGGTAATGC 990
Db 1020 AAGGGTTATTGTTCTTTTATATTAATTCGTTTGTCTTTCAGAAAATGTTTATAGGTAATGC 1079
QY 991 ATAAGACTATGCAATATTTTATATTAATTCATAGTATTAATGTTGTTTAAAGTTGTTGTAC 1050
Db 1080 ATAAGACTATGCAATATTTTATATTAATTCATAGTATTAATGTTGTTTAAAGTTGTTGTAC 1139
QY 1051 TTTGAAAAAATAA 1064
Db 1140 TTTGAAAAAATAA 1153

RESULT 5

ABST0424
ID ABST0424 standard; cdna; 1154 BP.

XX AC ABST0424;

XX DT 27-NOV-2002 (first entry)

XX DE Human bone remodelling gene #81.

XX KW Bone remodelling; osteoporosis; human; gene; ss.

XX OS Homo sapiens.

XX PN US6426186-B1.

XX PD 30-JUL-2002.

XX PF 18-JAN-2000; 2000US-0484970.

XX PR 18-JAN-2000; 2000US-0484970.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Jones KA, Volkmath W, Walker MG;

XX PF 2002-673014/72.

XX A combination of polynucleotides which are co-expressed with genes
PT known to be involved in bone remodeling and osteoporosis are useful in
PT an array for the diagnosis of bone remodeling and osteoporosis
PT associated disorders -

XX Claim 1; Column 239-242; 206pp; English.

XX The invention relates to a combination comprising a number of
CC substantially purified and isolated polynucleotides which are
CC co-expressed with genes known to be involved in bone remodeling and
CC osteoporosis. The invention is used to diagnose disorders associated
CC with bone remodeling or osteoporosis. ABST0344-ABS70512 represent
CC human bone remodelling genes of the invention.

XX SQ Sequence 1154 BP; 367 A; 216 C; 285 G; 265 T; 21 other;
Query Match 76.4%; Score 825.2; DB 24; Length 1154;
Best Local Similarity 97.9%; Pred. No. 1.3e-178;
Matches 836; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 211 GCTCGAGAGCTGGCAACAATAATCAAGAAACGTTTAAAGGAATTTGATGATCTACGA 270
Db 301 GCTCGAGAGCTGGCAACAATAATCAAGAAACGTTTAAAGGAATTTGATGATCTACGA 360
QY 271 AAAATATAAGAAAGAGATGATTTAAACCAAGAAACGTTTAAAGGAATTTGATGATCTACGA 330
Db 361 AAAATATAAGAAAGAGATGATTTAAACCAAGAAACGTTTAAAGGAATTTGATGATCTACGA 420
QY 331 AGCAGCTAAATTAATAGTCAAGAAATTTGGGAGATGAAAAAATACAGATTTGTACAAATGCT 390
Db 421 AGCAGCTAAATTAATAGTCAAGAAATTTGGGAGATGAAAAAATACAGATTTGTACAAATGCT 480
QY 391 CGAATTTGGTGGAAATTCGGGCAAGACAAATGGAAGTTTACACTCAGTGTGTTTCAAGATCC 450
Db 481 CGAATTTGGTGGAAATTCGGGCAAGACAAATGGAAGTTTACACTCAGTGTGTTTCAAGATCC 540
QY 451 TCGTGAAGTGAACGAGCCTCAGATTAAGCAAGATGGAATTCAGGCCAACCAAGATGATC 510
Db 541 TCGTGAAGTGAACGAGCCTCAGATTAAGCAAGATGGAATTCAGGCCAACCAAGATGATC 600
QY 511 TTCAGAAGACCCCGCAGGACCGGACCAAGTGAAGCCGTTTATGTCACATGTCAAA 570
Db 601 TTCAGAAGACCCCGCAGGACCGGACCAAGTGAAGCCGTTTATGTCACATGTCAAA 660
QY 571 TGGGATTGAAGACTGTGATGATCAGCCACCTTAAGAAAAGAAATCCAAGTCAGCAAGAA 630
Db 661 TGGGATTGAAGACTGTGATGATCAGCCACCTTAAGAAAAGAAATCCAAGTCAGCAAGAA 720
QY 631 AAAGAAACGCTCCAGGCCAAAGCAGGAAAGGGAAGCTTCACCTGTGAGTTTGCATATAGA 690
Db 721 AAAGAAACGCTCCAGGCCAAAGCAGGAAAGGGAAGCTTCACCTGTGAGTTTGCATATAGA 780
QY 691 TCCTAATGAACCTACATACCTGTTATGCAACCAAGTGTCTTATGGGAGATGATAGGATG 750
Db 781 TCCTAATGAACCTACATACCTGTTATGCAACCAAGTGTCTTATGGGAGATGATAGGATG 840
QY 751 TGACATGAACAGTGTCCCAATGAAATGTTTCACTTTTCACTTACCTATATA 810
Db 841 TGACATGAACAGTGTCCCAATGAAATGTTTCACTTTTCACTTACCTATATA 900
QY 811 ACCAAAGGGGAAATGTTATGCCCCAAGTGCAGGGGAGATTAATGAGAAAACAATGACAA 870
Db 901 ACCAAAGGGGAAATGTTATGCCCCAAGTGCAGGGGAGATTAATGAGAAAACAATGACAA 960
QY 871 AAGTACTGAAAAGACAAAAGGATAGAGATCGAGTGTAGTAAGGCCATCCACATTTTA 930
Db 961 AAGTACTGAAAAGACAAAAGGATAGAGATCGAGTGTAGTAAGGCCATCCACATTTTA 1020
QY 931 AAGGGTTATTGTTCTTTTATATTAATTCGTTTGTCTTTCAGAAAATGTTTATAGGTAATGC 990
Db 1021 AAGGGTTATTGTTCTTTTATATTAATTCGTTTGTCTTTCAGAAAATGTTTATAGGTAATGC 1080
QY 991 ATAAGACTATGCAATATTTTATATTAATTCATAGTATTAATGTTGTTTAAAGTTGTTGTAC 1050
Db 1081 ATAAGACTATGCAATATTTTATATTAATTCATAGTATTAATGTTGTTTAAAGTTGTTGTAC 1140
QY 1051 TTTGAAAAAATAA 1064
Db 1141 TTTGAAAAAATAA 1154

RESULT 6

AAC28459
ID AAC28459 standard; cdna; 346 BP.

XX AAC28459;
AC AAC28459;

QY 970 AAAATGTTTAGGTAATGCAATGACTATGCAATTAATTTTAATCATTAGTATTAATG 1029
 Db |||||||
 85 AAAATGTTTAGGTAATGCAATGACTATGCAATTAATTTTAATCATTAGTATTAATG 26
 QY 1030 GTGTATTAAAGTGTGTACTTTG 1054
 Db |||||||

RESULT 8

AAA53790

ID AAA53790 standard; cDNA; 2817 BP.

XX

AC AAA53790;

XX DT 19-DEC-2000 (first entry)

XX

XX DE Murine P37ING1 coding sequence.

XX

KW p53; tumour; cancer; detection; antibody; hybridisation; exon 1b;
 KW ING1; ing1; p37ING1; p37ING1; oncogene; gene therapy; diagnosis;
 KW proliferation disorder; transformation; transformed cell; mouse; ds.

XX

XX OS Mus musculus.

XX

XX FH Key Location/Qualifiers

XX FT CDS 847..1686

XX FT /*tag= a

XX FT /product= P37ING1 polypeptide

XX

XX PN W0200046370-A1.

XX

XX PD 10-AUG-2000.

XX

XX PF 04-FEB-2000; 2000WO-US02959.

XX

XX PR 04-FEB-1999; 99US-0118941.

XX

XX PA (UNII) UNIV ILLINOIS FOUND.

XX

XX PI Gudkov A, Zeremski M, Gurova KV, Grigorian IA;

XX

XX DR WPI; 2000-491278/43.

XX

XX DR P-PSDB; AAY97242.

XX

PT Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing
 PT and treating cancer, comprises contacting sample with isolated nucleic
 PT acid comprising sequence of exon 1b and detecting hybridized products

XX

XX PS Disclosure; Fig 11; 134pp; English.

XX

XX CC Mutations in or loss of the p53 gene occur in more than 50% of

XX

XX CC human tumours and tumour cell lines, but functional inactivation of

XX

XX CC the p53 pathway occurs in a much larger proportion of tumours. In

XX

XX CC many cases the mechanism of functional inactivation of the p53 gene

XX

XX CC remains unknown but p53 has been found to act in cooperation with

XX

XX CC ING1. Functional cooperation between ING1 and p53 suggested that

XX

XX CC ING1 encoded a tumour suppressor protein that functioned within the

XX

XX CC p53 pathway. This data suggested a possible role for ING1 in head

XX

XX CC and neck cancers and chromosomal location of the ING1 placed it

XX

XX CC within a region that is frequently rearranged in head and neck

XX

XX CC cancers. Large scale analysis of tumours involving ING1 has not

XX

CC proliferation or transformation of those cells. Thus detecting a
 CC nucleic acid encoding exon 1b of ing1 by hybridisation with an
 CC isolated nucleic acid having the sequence of exon 1b of ing1
 CC or its antisense sequence can identify individuals expressing the
 CC oncogenic form of ing1. Novel peptide sequences taken from the 104
 CC N-terminal peptide of p37ING1 can also be used to raise antibodies
 CC that can also be used in detection methods for the p37ING1 variant.
 CC The polypeptides may be useful in gene therapy for treatment of cell
 CC proliferation disorders, especially cancers and for diagnosing and
 CC studying cancers.
 XX
 SQ Sequence 2817 BP; 670 A; 711 C; 846 G; 590 T; 0 other;

Query Match 23.5%; Score 253.6; DB 21; Length 2817;
 Best Local Similarity 60.3%; Pred. No. 5.8e-48;
 Matches 490; Conservative 0; Mismatches 289; Indels 33; Gaps 3;

QY 116 ACCGGGAGCGGAGCCGGCTGCTCACCTGCTACGTGCGAGGACTACCTTGTAGTGGTGGAG 175

Db |||||||

862 AACGGGAGCAGATCCACCTGGTGA---ACTATGTGAGGATTACCTGGGACTCAATCGAG 918

QY 176 TCGCTCCCCCAGACATGAGAGGACGCTGCTGCTGCGAGAGCTGGGACACAAATAT 235

Db |||||||

919 TCACCTGCTTTTCACCTGCGAGGAGACGCTCTCGCTGATGCGGAGATCGACGCCAATATC 978

QY 236 CAAGAAACGTTAAAGGAAATTTGATGATGCTTACGAAAAATATAGAAAGAGATGATTTA 295

Db |||||||

979 CAAGAGATCCTGAGAGGCTGGACGACTACTATGAGAGTTCAACGGGAGACAGACGGC 1038

QY 296 AACCAAGAAACGCTCTACAGCAGCTTCTCCAGAGAGCAGCTAATTAATAGTCAAGATTTG 355

Db |||||||

1039 ACCCAGAGCGCGGGTACTGCACTGCACTCCAGAGGGCCCTGATCCGACCCAGGAGCTA 1098

QY 356 GGAGATGAAATAATACAGATTGTTACAAATGCTCGAATTGTTGGAATTCGGGCAAGA 415

Db |||||||

1099 GCGATGAGAAGATCCAGATCGTGAGTCAGTGGTGAGCTGGTGAGAACCCGACGAGA 1158

QY 416 CAAATGGGATTACACTCACAGTGTGTTTCCAAAGATCTCTCTGAAA----- 458

Db |||||||

1159 CAGTGGACAGTCACGTGGAGCTCTTTCGAAGACACACAGGACATCATGACGGCAGCTGGT 1218

QY 459 -----GTGAACGAGCCTCAGATAAAGCAAGAGATGGATTCCAGCCCAACAGAAAGATCT 511

Db |||||||

1219 GGCAGCGGCAAGCGCGGCGCAGGACAAGTCGAAGATGAGGCCATCACACAGGCGAGATAAG 1278

QY 512 TCAGAA-----GACCCCGAGGCGGAGCGGACGAGTGAAGCCGCTGATTATGTCAATG 565

Db |||||||

1279 CCGAATAACAAGCGGTCCAGAGGCGCAGGAGCAAAACAATGAGAAATCGAGAGAACGGGTGCAAT 1338

QY 566 GCAATGGGATTGAAGACTGTGATGATCAGCCACCTTAAAGAAAGAAATCCAAAGTCAGCA 625

Db |||||||

1339 AATCAGCAGCATGATGACATACCTCAGGAACGCCCAAGGAGAGAAAGCAAAACCTCA 1398

QY 626 AAGAAAAAGAAACGCTCCAGGCGCAAGCAGGAAAGGAAAGCTTCACCTGTGTGAGTTTGA 685

Db |||||||

1399 AAGAAGAAGAAACGCTCCAGGCGCAAGCAGGAGGAGGAGCGTCTCTGCGGACCTTCCC 1458

QY 686 ATAGATCTTAATGAACCTTACATCTCTTATGCAACCAAGTGTCTTATGGGAGAGATGA 745

Db |||||||

1459 ATCGACCCCAACGAGGCCACGCTACTCTGTGTCAACACGAGTCTCTTACGCGGAGATGATC 1518

QY 746 GGATGTGCAANTGACAGTGTCCAATGATGGTTTCACTTTTCATGTGTTTCACTTACC 805

Db |||||||

1519 GCGTGTGACACAGCAAGATGCCCCCATCGAGTGGTTTCCACTTCTCTCGGTGGGGCTCAAC 1578

QY 806 TATAAACCAAGGGGAAATGGTATTGCCCAAGTCAGGGGAGATATAGAGAAAAAATG 865

Db |||||||

1579 CATTAACCAAGGGGCAAGTGGTACTGCCCCCAAGTGGCGTGGGAGAGCGAGAACCATG 1638

QY 866 GACAAAAGTACTGAAAGACAAAAAGGATAG 897

Db |||||||

1639 GACAAAGCCCTGAGAAAGTCCCAAGAAAGAGAG 1670

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OS Homo sapiens.
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FT /product= "cancer associated antigen"
XX W0200147959-A2.
XX
XX 05-JUL-2001.
XX
XX 29-NOV-2000; 2000WO-US42334.
XX
XX 30-NOV-1999; 99US-0451739.
XX 24-OCT-2000; 2000US-0602362.
XX
XX (LJDM-) LUDWIG INST CANCER RES.
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
XX WPI; 2001-441706/47.
XX P-PSDB; AAB84698.
XX
XX Isolated cancer associated nucleic acid molecule identified by SEREX
XX (serological identification of antigens by recombinant expression
XX cloning) technique, useful in nucleic acid based therapies to treat
XX cancer -
XX
XX Claim 1; Page 43-44; 62pp; English.
XX
XX The present sequence encodes a human cancer associated antigen.
XX The sequence is a variant of the ING1 gene, which is a tumour
XX suppressor gene candidate. The cancer associated antigen polynucleotides
XX and polypeptides are useful for screening for the possible presence of
XX a pathological condition in a subject such as cancer. The cancer
XX associated antigen polypeptides are useful for producing vaccines.
XX
XX Sequence 1533 BP; 336 A; 431 C; 521 G; 244 T; 1 other;
XX
XX Query Match 21.9%; Score 236; DB 22; Length 1533;
XX Best Local Similarity 58.9%; Pred. No. 4.8e-44;
XX Matches 462; Conservative 0; Mismatches 290; Indels 32; Gaps 2;
XX
XX 145 CTACGTGCAGGACTACCTTGAGTCGTCGGAGTCGTCGCCACGACATGCAGAGGAACGT 204
XX 492 CTATGTGGAGGACTACTCGACTCCATCGAGTCGCCCTTCGACTTCGAGAAATGT 551
XX
XX 205 GTCTGTGCTCGGAGAGCTGGACAAACAAATATCAAGAAACGTTAAAGGAAATTCATGATGT 264
XX
XX 552 CTGCTGTATCGGGAGATCGACCGGAAATACCAAGAGATCCTGAAGAGCTAGACGATG 611
XX
XX 265 CTACGAAAAATATAGAAAGAAGATGATTTAAACCCAGAGAAACGCTCTACAGCAGCTTCT 324
XX
XX 612 CTACGAGCGCTTCAGTCGCGAGACAGACGGCGGCGCAGAGCGCGGATGTCACGTGTGT 671
XX
XX 325 CCAGAGAGCACTAATTAATAGTCAAGATTTGAGAGATGAAATAACAGATTGTTACACA 384
XX
XX 672 GCAGCGCGGCTGATCCGACGACGAGGAGCTGGGCGCAGAGAGATCCAGATCGTGAGCCA 731
XX
XX 385 AATGCTCGAATTCGTGAAATCGGCAACAAATGGAGTTACACTCACAGTGTTCGA 444
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XX 732 GATGTTGGAGCTGTTGGAGAACCGCGCGGAGGTGGACGACGCTGGAGCTGTTCGA 791
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XX 445 AGATC-----CTGCTGAAAGTGAACGAGCCTCAG 473
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Db 792 GCGCAGCAGGAGCTGGGCGACACAGCGGGCAACACGCGGCAAGGCTGGCGCGACAGGCC 851
QY 474 ATAAAGCAAGATGGATTCCAGCCACACAGAAAGATCTTCAAGAAAGACCCCGCAGGCAGC 533
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QY 534 GGACCAAGTGAAGCCGCTGATTTATGTCAATGGCAAAATGGGATTTGAAGACTGTGATGATC 593
Db 911 GCAACAAACGAGAACCGTGAGAACCGCTCCAGCAACCCACGACCAACGACGCGGCGCTCGG 970
QY 594 AGCCACCTAAAGAAAGAAATCCAGTCAAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 653
Db 971 GCACACCCCAAGGAGAGAGGCGCAAGCTCCAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1030
QY 654 AGGAAGGGAAGCTTCACCTGTTGAGTTTGGCAATAGATCCTTAATGAACCTACATACTGCT 713
Db 1031 CGGAGCGAGAGGGTCCCTCGGACCTCCCATCGACCCCAACGAAACCCACGACTGTC 1090
QY 714 TATGCAACCAAGTGTCTTATGGGAGATGATAGGATGTGACAAATGAACAGTGTCCAAATTG 773
Db 1091 TGTGCAACCAAGTGTCTTATGGGAGATGATCGGTGCGACAAACGACGAGTGCCCATCG 1150
QY 774 AATGTTTCACCTTTTCATGTTTCACTTACCTATAAACCAAGGGGAAATGTTATGCC 833
Db 1151 AGTGGTTCCACTTCTCGTGGGCTCAATCATAAACCCCAAGGGCAAGTGGTACTGTC 1210
QY 834 CAAAGTGCGAGGAGATATGAGAAACAAATGACAAAGAAAGTACTGAAAGACAAAAAGG 893
Db 1211 CCAAGTGCGGGGAGAGACGAGAGACCATGGACAAAGCCCTGGAGAAATCCAAAAAG 1270
QY 894 ATAG 897
Db 1271 AGAG 1274

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RESULT 11
ABK86977
ID ABK86977 standard; cDNA; 2897 BP.
XX
AC ABK86977;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human inhibitor of growth 1 (ING1) isoform, p33ING1b, cDNA.
XX
KW Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1;
KW ING1; tumour suppressor; cell cycle; breast tumour; lymphoid malignancy;
KW cell growth; anti-ING1; CAB; isoform; diagnosis; tumour; antigen;
KW p33ING1b.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 873..1712
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FT /product= "p33ING1b"
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XX US2002039735-A1.
XX
XX 04-APR-2002.
XX
XX 04-JUN-2001; 2001US-0874347.
XX
XX 02-JUN-2000; 2000US-208829P.
XX 26-FEB-1999; 99US-0258372.
XX 15-NOV-1996; 96US-0751230.
XX 08-DEC-1995; 95US-0569721.
XX 22-MAR-2000; 2000US-0532868.
XX
XX (RIAB/) RIABOWOL K T.
XX (BOLA/) BOLAND D.
XX
XX Riabowol KT, Boland D;

```


CC an identical C-terminal fragment to INGI but an additional 104
CC N-terminal amino acids. The newly discovered protein has been
CC designated p37ING1 (Wild type: p33ING1). p37ING1 has the
CC characteristics of an oncogene. When overexpressed in cells (even
CC those expressing wild type p53) p37ING1 is able to cause
CC proliferation or transformation of those cells. Thus detecting a
CC nucleic acid encoding exon 1b of ingi by hybridisation with an
CC isolated nucleic acid having the sequence of exon 1b of ingi
CC or its antisense sequence can identify individuals expressing the
CC oncogenic form of ingi. Novel peptide sequences taken from the 104
CC N-terminal peptide of p37ING1 can also be used to raise antibodies
CC that can also be used in detection methods for the p37ING1 variant.
CC The polypeptides may be useful in gene therapy for treatment of cell
CC proliferation disorders, especially cancers and for diagnosing and
CC studying cancers.
XX
SQ Sequence 1835 BP; 541 A; 387 C; 468 G; 439 T; 0 other;

Query Match 18.3%; Score 197.2; DB 21; Length 1835;
Best Local Similarity 58.5%; Pred. No. 3.7e-35;
Matches 399; Conservative 0; Mismatches 253; Indels 30; Gaps 2;

QY 246 TAAAGGAATTTGATGCTTCCAGAGAGCACTAATTAATAGTCAAGAAATGGGAGATGAAA 305
Db 7 TGAAGGAGCTGGAGCACTACTATGAGAAGTTCAAACGGGAGACAGACGGCACCAGAAGC 66

QY 306 AACGCTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAAATGGGAGATGAAA 365
Db 67 GCGGGTACTGCTACTGCTATCCAGAGGGCCCTGATCCGAGCCAGGAGCTAGGCGATGAGA 126

QY 366 AATAACAGATTGTTACAAAATCTCGAATTTGGTGGAAATCGGGCAAGCAAAATGGAGT 425
Db 127 AGATCCAGATCGTGAGTGCAGATGGTGAGCTGGTGGAGAACCGCAGCAGACAGGTGGACA 186

QY 426 TACACTCACAGTGTTCACAGATCTCTGTGAAA-----GTGA 462
Db 187 GTCCGTGGAGTCTTCGAGACACACAGGACATCATGTCAGCGCACTGTGGCAGCGGCA 246

QY 463 ACAGAGCTCAGATAAAGCAAGATGATTCAGCCCAACAGAAAGATCTTCAAGAGAGC- 521
Db 247 AGCGGGCCAGGCAAGTCCGAGAGTGGAGCCATCACAGGCGAGATAGCCGATTAACA 306

QY 522 -----CCGCGAGCGGAGCCAGTGAAGCCGCTGATTTATGTCTACATGGCAAAATGGGA 575
Db 307 AGCGGTCCAGAGGCGAGCAACAATGAGAAATCGAGAGAACGGTCTGAATATCATCGACC 366

QY 576 TTGAAGACTGTGATGATCAGCCACTTAAGAAAGAAATCCAAAGTCAGCAAGAAAGAA 635
Db 367 ATGATGACATCACTCAGGAACGCCCAAGGAGAAAGCAAAACCTCAAAAGAAAGA 426

QY 636 AACGCTCCAGGCGCAAGCAGGAAGGAAGCTTCACCTGTGAGTTTGGCAATAGATCCTA 695
Db 427 AACGCTCCAGGCGCAAGCAGGAGGAAGCGTCTCTGCGGACCTTCCATCGACCCCA 486

QY 696 ATGAACCTCATCATCTGTTATGCAACCAAGTGTCTTATGGGAGATCATAGATGTGACA 755
Db 487 ACCGAGCCCGTACTGCTGTGCAACAGGTCTCTTACGGGAGAGATCGGCTGTGACA 546

QY 756 ATGAACAGTGTCAAATGTAATGTTTCATCTTTTCATGTGTTTCATCTAATAAACCAA 815
Db 547 ACCAGCAATGCCCATCGAGTGTTCACCTTCTCTCGGTGGGCTCAACCATAAACCAA 606

QY 816 AGGGGAATGGTATTCGCCCAAGTCGAGGAGATTAATGAGAAACAAATGGACAAAGTA 875
Db 607 AGGGCAAGTGGTACTGCCCAAGTGGCGGTGGGAGAGCGAGAACCATGGACAAAGCCC 666

QY 876 CTGAAAAGACAAAAAGGATAG 897
Db 667 TGGAGAGTCCAGAAGAGAG 688

ID AAH28479 standard; DNA; 1143 BP.
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AC AAH28479;
XX
DT 17-SEP-2001 (first entry)
XX
DE Nucleotide sequence of a human cancer associated antigen.
XX
KW Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.
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OS Homo sapiens.
XX
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XX
PN WO200147959-A2.
XX
PD 05-JUL-2001.
XX
PF 29-NOV-2000; 2000WO-US42334.
XX
PR 30-NOV-1999; 99US-0451739.
PR 24-OCT-2000; 2000US-0602362.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
XX
DR WPI; 2001-441706/47.
XX
DR P-PSDB; AAB84697.
XX
PT Isolated cancer associated nucleic acid molecule identified by SRREX
PT (serological identification of antigens by recombinant expression
PT cloning) technique, useful in nucleic acid based therapies to treat
PT cancer -
XX
PS Example 4; Page 44; 62pp; English.
XX
CC The present sequence encodes a human cancer associated antigen.
CC The sequence is the wildtype of the INGI gene, which is a tumour
CC suppressor gene candidate. The cancer associated antigen polynucleotides
CC and polypeptides are useful for screening for the possible presence of
CC a pathological condition in a subject such as cancer. The cancer
CC associated antigen polypeptides are useful for producing vaccines.
XX
SQ Sequence 1143 BP; 289 A; 291 C; 366 G; 197 T; 0 other;

Query Match 17.0%; Score 183.8; DB 22; Length 1143;
Best Local Similarity 57.0%; Pred. No. 3.6e-32;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;

QY 237 AAGAAACGTTAAAGGAATTTGATGCTTACGAAATAATAGAAAGAGATGATTTAA 296
Db 194 AACAGATCTCTGAAGGAGCTAGACGAGTGTACGAGCGCTTCAGTCGAGACAGACGGGG 253

QY 297 ACCAGAGAAACGCTTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGATTTG 356
Db 254 CCAGAAAGCGCGGATGCTGCACTGTGTGACGCGCGCTGTATCCGACCCAGGAGCTGG 313

QY 357 GAGATGAAAAATACAGATTGTTACAAATGCTCGAATTTGGTGGAAATTCGGGCAAGAC 416
Db 314 GCGACGAGAGATCCAGATCGTGAGCCAGATGTTGGAGCTGTGGAGACCCGACCGGC 373

QY 417 AAATGGAGTTACACTCACAGTGTTCCTCAAGATC----- 449
Db 374 AGGTGGACAGCCACGTTGGAGTGTTCGAGCGCAGCAGGAGCTGGGCGACACAGTGGGCA 433

XX AAV62285;
 XX 18-JAN-1999 (first entry)
 XX Partial INGI partial cDNA sequence.
 XX INGI gene; p33ING1; human; apoptosis; cell death; breast cancer;
 KW brain tumour; gene therapy; tumour suppressor; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 109..741
 FT /*tag= a
 FT
 XX W09844102-A2.
 XX 08-OCT-1998.
 XX 26-MAR-1998; 98WO-CA00277.
 XX 27-MAR-1997; 97US-0828158.
 XX (UYTE-) UNIV TECHNOLOGIES INT INC.
 XX Garkavtsev I, Helbing CC, Johnston RN, Riabowol K;
 XX WPI: 1998-542700/46.
 DR P-PSDB; AAW79674.
 XX
 PT Modulating eukaryotic apoptosis by increasing p33ING1 activity -
 PT using p33ING1 derivatives, to induce apoptosis in cancer cells, and
 PT in the investigation of apoptotic pathways
 XX
 PS Example 2; Fig 2; 66pp; English.
 XX
 CC This is the nucleotide sequence of a human INGI (INHIBITOR of
 CC Growth) partial cDNA clone that codes for a p33ING1 polypeptide
 CC (see AAW79674), a novel inhibitor of cell growth and a candidate
 CC tumour suppressor. INGI is a new gene that is expressed in normal
 CC mammary epithelial cells, but which is expressed only at lower
 CC levels in several cancerous mammary epithelial cell lines and is
 CC not expressed in many primary brain tumours. To isolate INGI, a
 CC subtractive hybridisation of breast cancer cell line cDNAs was
 CC performed with cDNA from normal mammary epithelial cells, and
 CC subtracted cDNAs were cloned into retrovirus vector pLNCX.
 CC Following passage through a packaging line, normal mouse mammary
 CC epithelial cells were infected, and infected cells were injected
 CC into nude mice. Putative transforming fragments from tumours were
 CC isolated by PCR (see AAV62290-91) and subcloned into LNCX. An INGI
 CC fragment was obtained and used to screen normal human fibroblast
 CC and HeLa cell cDNA libraries. 2 Clones were sequenced to obtain
 CC the partial INGI sequence. The complete cDNA sequence (see
 CC AAV62292) was obtained by RACE. A claimed method to potentiate
 CC apoptosis in a eukaryotic cell involves administering an active
 CC p33ING1 peptide or an oligonucleotide encoding such as a peptide.
 CC A claimed method for inhibiting apoptosis in a eukaryotic cell
 CC involves administering an antisense oligonucleotide. Also claimed
 CC are a method for determining the apoptotic characteristics of a
 CC eukaryotic cell, an assay for determining the level of p33ING1
 CC activity in a eukaryotic cell, and an isolated eukaryotic cell
 CC substantially free of p33ING1 biological activity. The invention
 CC discloses INGI derivatives or variants that may be used to induce
 CC apoptosis in eukaryotic cancer cells.
 XX
 SQ Sequence 1902 BP; 574 A; 390 C; 462 G; 476 T; 0 other;

Query Match 17.0%; Score 183.8; DB 19; Length 1902;
 Best Local Similarity 57.0%; Pred. No. 4.3e-32;
 Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;

QY 237 AAGAACGTTAAAGGAAATTGATGATCTACGAAAAATATAGAAAGAGATGATTAA 296

Db 35 AACAGATCCTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCGCGAGACAGACGGGG 94
 QY 297 ACCAGAAGAAACGCTCTACAGCAGCTTCTCCAGAGACACTAATTAATAGTCAAGAAATTGG 356
 Db 95 CCAGAAGCGCGGATGCTGCACTGTGTGACGGCGCTGATCCGACGACGAGAGCTGG 154
 QY 357 GAGATGAAAAAATACAGATTGTTTACACAAATGCTCGAATTGGTGGAAAAATCGGGCAGAC 416
 Db 155 GCGACGAGAAGATCCAGATCGTGTGAGCTGTGTGAGCTGTGTGGAGAACCGGCACGCGGC 214
 QY 417 AAATGGAGTTACTCACTCAAGTGTTCCTCAAGATC----- 449
 Db 215 AGGTGGACACCCACGCTGGAGCTGTTTCGAGGCGCAGCAGGAGCTGGGCGCACACAGTGGCA 274
 QY 450 -CTGCTGAAAGTGAACGAGCGCTCAGATAAAGCAAAAGATGATTTCCAGCCCAACAGAAAGA 508
 Db 275 ACAGCGGCAAGTGTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCATGTCTGCAAGC 334
 QY 509 TCTTCAAGAA--GACCCCGCAGCGCAGCGACCGAGTGAAGAGCGGTGATTTATGTCAATGG 566
 Db 335 CCAACAGCAAGCGCTCACGGCGCAGCGCAACACGAGAACCGTGTAGAACGCGTCCAGCA 394
 QY 567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTTAAGAAAGAAATCCAAGTCAAGCAA 626
 Db 395 ACCACGACCACGACGACGCGCTCGGGCACACCCCAAGGAGAAGAGGCGCAAGACCTCCA 454
 QY 627 AGAAAAAGAAACGCTCCAGGCGCAGCAGGAAAGGAAAGCTTCACCTGTTGAGTTTGCAG 686
 Db 455 AGAAGAAGAAAGCGCTCCAAAGGCCAAGGCGGAGAGGCGTCCCTGCCGACCTCCCA 514
 QY 687 TAGATCCTTAATGAACCTCATACTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAG 746
 Db 515 TCGACCCCAACGAAACCCAGTACTGTCTGTGCAACCAAGGTCTCTATGGGAGATGATCG 574
 QY 747 GATGTGACAATGAAACAGTGTCCAAATGAAATGTTTTCATTTTCAATGTGTTTCACTTACCT 806
 Db 575 GCTGGGACAAACGACGAGTGCCTCCATCGAGTGGTTCCACTTCTCGTGGTGGGCTCAATC 634
 QY 807 ATAAACCAAGGGGAAATGGTATTGCCCAAGTGCAGGGGAGATATATGAGAAACATGG 866
 Db 635 ATAAACCCCAAGGGCAAGTGGTACTGTCCCAAGTGCAGGGGAGAGACGAGAACCATGG 694
 QY 867 ACAAAAGTACTGAAAAAGACAAAAAGGATAG 897
 Db 695 ACAAGCCCTGGAGAAATCCAAAAAGAGAG 725

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 Job time : 344 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2004, 16:38:42 ; Search time 3978 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1080	100.0	1080	9	AF053537	AF053537 Homo sapi
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4	1046	96.9	1078	6	AR213555	AR213555 Sequence
5	1046	96.9	1078	9	AB012853	AB012853 Homo sapi
6	839.8	77.8	843	9	HSJ76851	AJ006851 Homo sapi
7	838.4	77.6	840	6	AR213554	AR213554 Sequence
8	825.2	76.4	1154	6	AR220840	AR220840 Sequence
9	817.2	75.7	183317	9	HSING282	AF062748 Homo sapi
10	817.2	75.7	183317	9	AC107214	AC107214 Homo sapi
11	761.4	70.5	1001	10	AF078834	AF078834 Mus muscu
12	700.2	64.8	1262	10	BC050003	BC050003 Mus muscu
13	686.8	63.6	231311	2	AC132966	AC132966 Rattus no
14	686.8	63.6	245104	2	AC128348	AC128348 Rattus no
15	686.8	63.6	247796	2	AC094539	AC094539 Rattus no
16	686.8	63.6	255408	2	AC129658	AC129658 Rattus no
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21	332.2	30.8	346	6	BD052204	BD052204 Sequence
22	256.8	23.8	840	10	AF149820	AF149820 Mus muscu
23	253.6	23.5	1584	10	BC016573	BC016573 Mus muscu
24	253.6	23.5	2817	10	AF177757	AF177757 Mus muscu
25	239.2	22.1	423	9	HSING251	AF062747 Homo sapi
26	237.4	22.0	873	6	AR171884	AR171884 Sequence
27	237.4	22.0	911	9	AF044076	AF044076 Homo sapi
28	237.4	22.0	1533	9	AF149721	AF149721 Homo sapi
29	237.4	22.0	2444	9	AB024401	AB024401 Homo sapi
30	236	21.9	840	9	AF078835	AF078835 Homo sapi
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33	236	21.9	2897	9	AF181850	AF181850 Homo sapi
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36	199	18.4	184918	2	AC114608	AC114608 Mus muscu
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42	183.8	17.0	1074	9	AF149722	AF149722 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AX211560 1080 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 7 from Patent WO0159114.
ACCESSION AX211560
VERSION AX211560.1 GI:15523814
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Harris,C.C. and Nagashima,M.
TITLE Tumour suppressor Gene, p47ing3
JOURNAL Patent: WO 0159114-A 7 16-AUG-2001;

THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

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Best Local Similarity 100.0%; Pred. No. 1.2e-221;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Homo sapiens p33 (ING2) mRNA, complete cds.
DEFINITION AF053537
ACCESSION AF053537
VERSION AF053537.1 GI:9992837
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1080)
AUTHORS Nagashima,M., Shiseki,M., Miura,K., Hagiwara,K., Linke,S.P.,
Pedoux,R., Wang,X.W., Yokota,J., Riabowol,K. and Harris,C.C.
TITLE DNA damage-inducible gene p33ING2 negatively regulates cell
proliferation through acetylation of p53
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001)
MEDLINE 21396501
PUBMED 11481424
REFERENCE 2 (bases 1 to 1080)
AUTHORS Nagashima,M., Hagiwara,K., Minter,A.R. and Harris,C.C.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, 37 Convent Drive Bldg.37 Rm.2C01,
Bethesda, MD 20892, USA
FEATURES
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BASE COUNT      375 a   196 c   271 g   238 t
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Best Local Similarity 100.0%; Pred. No. 1.2e-221;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
BC030128LOCUS
DEFINITION

BC030128 Homo sapiens, 1141 bp mRNA linear PRI 20-MAY-2002
MGC:10524 IMAGE:3941655, mRNA, complete cds.

ACCESSION

BC030128

VERSION

BC030128.1 GI:20987212

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1141)

AUTHORS

Strausberg, R.

TITLE

Submitted (07-MAY-2002) National Institutes of Health, Mammalian

JOURNAL

Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

COMMENT

USA

COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk

COMMENT

Email: cgapbs-r@mail.nih.gov

COMMENT

Tissue Procurement: DCTD/DTp

COMMENT

CDNA Library Preparation: Rubin Laboratory

COMMENT

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

COMMENT

DNA Sequencing by: National Institutes of Health Intramural

COMMENT

Sequencing Center (NISC),

COMMENT

Gaithersburg, Maryland;

COMMENT

Web site: <http://www.nisec.nih.gov/>

COMMENT

Contact: nisc_mgc@nhgri.nih.gov

COMMENT

Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

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Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

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Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

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Hansen, N., Ho, S.-L., Karlins, E., Laric, P., Legaspi, R., Maduro, Q.L.,

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Masiello, C., Masteri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J.,

COMMENT

Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C.,

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Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A.,

COMMENT

Zhang, L.-H. and Green, E.D.

COMMENT

Clone distribution: MGC clone distribution information can be found

COMMENT

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

COMMENT

Series: IRAL Plate: 15 Row: m Column: 11

COMMENT

This clone was selected for full length sequencing because it

COMMENT

passed the following selection criteria: matched mRNA gi: 4504694.

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Location/Qualifiers

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1. 1141

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COMMENT

Query Match 99.4%; Score 1073; DB 9; Length 1141;

COMMENT

Best Local Similarity 100.0%; Pred. No. 3.8e-220;

COMMENT

Matches 1073; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

COMMENT

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LOCUS AR213555 1078 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 7 from patent US 6403785.
ACCESSION AR213555
VERSION AR213555.1 GI:23310822
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1078)
AUTHORS Nagata,M., Ozaki,K., Shimada,Y. and Horie,M.
TITLE Isolated DNA molecule encoding human TSC403
JOURNAL Patent: US 6403785-A 7 11-JUN-2002;
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Location/Qualifiers
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BASE COUNT 356 a 206 c 280 g 236 t
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Query Match 96.9%; Score 1046; DB 6; Length 1078;
Best Local Similarity 99.5%; Pred. No. 2.4e-214;
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RESULT	5
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LOCUS	AB012853 1078 bp mRNA linear
DEFINITION	Homo sapiens INGIL mRNA for INGILP, complete cds.
	PRI 18-MAR-1999

ACCESSION	AB012853
VERSION	AB012853.1
KEYWORDS	GI:4115554
SOURCE	ING11p.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (sites)
JOURNAL	Shimada, Y., Saito, A., Suzuki, M., Takahashi, E. and Horie, M. Cloning of a novel gene (ING1L) homologous to ING1, a candidate tumor suppressor
	Cytogenet. Cell Genet. 83 (3-4), 232-235 (1998)

235 (1998)
NOT prior art

COMMENT	FEATURES	source
Sequence updated (17-Apr-1998).	Location/Qualifiers	
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1. .1078	1. .1078	
/gene="INGIL"	/gene="INGIL"	
92. .934	92. .934	
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356 a	280 g	236 t
BASE COUNT		

QY 188 GACATGACAGAGAAACGTTGCTGCTGCGAGAGCTGGACAAACAAATATCAAGAAACGTTA 247
DB 121 GACATGACAGAGAAACGTTGCTGCTGCGAGAGCTGGACAAACAAATATCAAGAAACGTTA 180
QY 248 AAGGAAATTCATGATGCTCTACGAAATATTAAGAAAGAGATGATTTAAACACGAGAGAAA 307
DB 181 AAGGAAATTCATGATGCTCTACGAAATATTAAGAAAGAGATGATTTAAACACGAGAGAAA 240
QY 308 CGTCTACAGCAGCTTCTCCACAGAGAGCACTAAATTAATAGTCAAGAAATGGGAGATGAAAA 367
DB 241 CGTCTACAGCAGCTTCTCCACAGAGAGCACTAAATTAATAGTCAAGAAATGGGAGATGAAAA 300
QY 368 ATACAGATTTGTACAAATGCTCGAATTCGATTCGAAATTCGGAATAATCGGCAAGACAAATGGAGTTA 427
DB 301 ATACAGATTTGTACAAATGCTCGAATTCGATTCGAAATTCGGAATAATCGGCAAGACAAATGGAGTTA 360
QY 428 CACTCAGAGTGTTCAGAGATCTCTGTAAGTGAACGAGCTTCAGATAAGCAAGATG 487
DB 361 CACTCAGAGTGTTCAGAGATCTCTGTAAGTGAACGAGCTTCAGATAAGCAAGATG 420
QY 488 GATTCCAGCCAAACAGAAAGATCTTCAAGAGACCCCGCAGGAGCGACCTGTAAGAGC 547
DB 421 GATTCCAGCCAAACAGAAAGATCTTCAAGAGACCCCGCAGGAGCGACCTGTAAGAGC 480
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DB 481 CGTGATTTATGTACATGGCAATGGGATTTGAAGACTGTGATGATCAGCCACCTAAAGAA 540
QY 608 AAGAAATCCAGTCCAGAAAGAAAGAAACGCTCCAGGCCCAAGCAAGGAGGAGCT 667
DB 541 AAGAAATCCAGTCCAGAAAGAAAGAAACGCTCCAGGCCCAAGCAAGGAGGAGCT 600
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DB 601 TCACCTGTTGAGTTGCAATAGATCCTTAATGAACCTACATCTTATGCAACCAAGTG 660
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QY 788 TCATGTGTTTCACTTACCTATAAACCAAGGGGAAATGTTATGTTCCCAAGTGCAGGGGA 847
DB 721 TCATGTGTTTCACTTACCTATAAACCAAGGGGAAATGTTATGTTCCCAAGTGCAGGGGA 780
QY 848 GATAATGAGAAACAATGGACAAAGTACTGAAAGACAAAGAGTGAAGATCGAGG 907
DB 781 GATAATGAGAAACAATGGACAAAGTACTGAAAGACAAAGAGTGAAGATCGAGG 840

RESULT 8
AR220840
LOCUS AR220840 1154 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 81 from patent US 6426186.
ACCESSION AR220840
VERSION AR220840.1 GI:23327717
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1154)
AUTHORS Jones, K.A., Volkmut, W. and Walker, M.G.
TITLE Bone remodeling genes
JOURNAL Patent: US 6426186-A 81 30-JUL-2002;
FEATURES
Location/Qualifiers
1..1154
/organism="unknown"

BASE COUNT 367 a 216 c 285 g 265 t 21 others
ORIGIN

Query Match 76.4%; Score 825.2; DB 6; Length 1154;
Best Local Similarity 97.9%; Pred. No. 7e-167;
Matches 836; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 211 GCTGCGAGAGCTGGACAAACAAATATCAAGAAACGTTTAAAGGAAATTTGATGATCTACGA 270
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QY 271 AAAATATAAGAAAGAGATGATTTAAACCAAGAAACGTTTACAGCAGCTTCTCCAGAG 330
DB 361 AAAATATAAGAAAGAGATGATTTAAACCAAGAAACGTTTACAGCAGCTTCTCCAGAG 420
QY 331 AGCAGCTAAATTAATAGTCAAGAAATGGGAGATGAAAAATACAGATTTGTTACACAAATGCT 390
DB 421 AGCAGCTAAATTAATAGTCAAGAAATGGGAGATGAAAAATACAGATTTGTTACACAAATGCT 480
QY 391 CGAATTTGTTGAAAAATCGGGCAAGACAAATGGAGTTTACACTCACAGTGTTTCCAAAGATCC 450
DB 481 CGAATTTGTTGAAAAATCGGGCAAGACAAATGGAGTTTACACTCACAGTGTTTCCAAAGATCC 540
QY 451 TGCTGAAAGTGAACGAGCCCTCAGATAAAGCAAGATGGATTTCCAGCACAACCAAGAAATC 510
DB 541 TGCTGAAAGTGAACGAGCCCTCAGATAAAGCAAGATGGATTTCCAGCACAACCAAGAAATC 600
QY 511 TTCAAGAAAGACCCCGCAGCAGCGACCTGTAAGAGCCGCTGATTTATGTCACATGCAAAA 570
DB 601 TTCAAGAAAGACCCCGCAGCAGCGACCTGTAAGAGCCGCTGATTTATGTCACATGCAAAA 660
QY 571 TGGGATTTGAAGACTGTGATGATCAGCCACCTTAAAGAAAGAAATCCAAAGTCAGCAAGAA 630
DB 661 TGGGATTTGAAGACTGTGATGATCAGCCACCTTAAAGAAAGAAATCCAAAGTCAGCAAGAA 720
QY 631 AAAGAAACGCTCCAGGCCCAAGCAAGGAGGAGCTTCACTGTTGAGTTTGCATATAGA 690
DB 721 AAAGAAACGCTCCAGGCCCAAGCAAGGAGGAGCTTCACTGTTGAGTTTGCATATAGA 780
QY 691 TCCTAATGAACCTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATGAGTG 840
DB 781 TCCTAATGAACCTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATGAGTG 840
QY 751 TGCAATGAACAGTGTCCAAATTTGAATGGTTTCACTTTTCATGTTTTCATCTTACCTATATA 810
DB 841 TGCAATGAACAGTGTCCAAATTTGAATGGTTTCACTTTTCATGTTTTCATCTTACCTATATA 900
QY 811 ACCAAAGGGGAAATGTTATGTTCCCAAGTGCAGGGGAGATTAAGAAAAACAATGACAAA 870
DB 901 ACCAAAGGGGAAATGTTATGTTCCCAAGTGCAGGGGAGATTAAGAAAAACAATGACAAA 960
QY 871 AAGTACTGAAAGACAAAGAAAGATAGAGATCGAGGTAGTAAAGCCCATCCACATTTTA 930
DB 961 AAGTACTGAAAGACAAAGAAAGATAGAGATCGAGGTAGTAAAGCCCATCCACATTTTA 1020
QY 931 AAGGGTTATTGTTCTTTTATATAATTTGTTTTCCTTTTCAGAAAAATGTTTATGGGTAATGC 990
DB 1021 AAGGGTTATTGTTCTTTTATATAATTTGTTTTCCTTTTCAGAAAAATGTTTATGGGTAATGC 1080
QY 991 ATAAGACTATGCAATAATTTTAAATCATTAGTATTAATAGTGTATTAAAGTGTGTTGATC 1050
DB 1081 ATAAGACTATGCAATAATTTTAAATCATTAGTATTAATAGTGTATTAAAGTGTGTTGATC 1140
QY 1051 TTTGAAAAAATAA 1064
DB 1141 TTTGAAAAAATAA 1154

RESULT 9
HSING252
LOCUS
DEFINITION Homo sapiens p33 (ING2) gene, exon 2, complete sequence; and
ACCESSION AF062748
VERSION AF062748.1 GI:9992841
KEYWORDS
SEGMENT 2 of 2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 974)
Nagashima, M., Hagiwara, K., Minter, A.R. and Harris, C.C.
Direct Submission
Submitted (01-MAY-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, 37 Convent Dr. Bldg. 37, Rm. 2C26,
Bethesda, MD 20892, USA

FEATURES

source 1. .974
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/evidence=experimental
BASE COUNT 348 a 156 c 205 g 265 t
ORIGIN

Query Match 75.7%; Score 817.2; DB 9; Length 974;
Best Local Similarity 99.8%; Pred. No. 3.6e-165;
Matches 819; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 117 TTTTGTAGAACGTTAAAGGAAATTTGATGTCTACGAAAAATATAAGAAAGAGATGAT 176
QY 293 TTAACACGAGAAACGTTACAGCAGCTTCTCCAGAGACACTAATTAATAGTCAAGAA 352
DB 177 TTAACACGAGAAACGTTACAGCAGCTTCTCCAGAGACACTAATTAATAGTCAAGAA 236
QY 353 TTGGGAGATCAAAAATACAGATTGTACACAAATCTCGAATTCGTGGAAATCGGCA 412
DB 237 TTGGGAGATCAAAAATACAGATTGTACACAAATCTCGAATTCGTGGAAATCGGCA 296
QY 413 AGACAAATGAGATTACACTCACAGTGTCTCCAGATCTCTGCTGAAAGTGAACGAGCTCA 472
DB 297 AGACAAATGAGATTACACTCACAGTGTCTCCAGATCTCTGCTGAAAGTGAACGAGCTCA 356
QY 473 GATAAGCAAGATGAGATTCCAGCCAAACGAAAGATCTTCAAGAAAGACCCCGCAGCGAG 532
DB 357 GATAAGCAAGATGAGATTCCAGCCAAACGAAAGATCTTCAAGAAAGACCCCGCAGCGAG 416
QY 533 CGGACCACTCAAGCCGCTGATTTATCTCATCGCAATGGGATTCAGACTGTGATGAT 592
DB 417 CGGACCACTCAAGCCGCTGATTTATGTTCATCGCAATGGGATTCAGACTGTGATGAT 476
QY 593 CAGCCACCTAAAGAAAGAAATCCAAAGTCAGCAAGAAAGAAAGAAAGCTCCAGAGGCAAG 652
DB 477 CAGCCACCTAAAGAAAGAAATCCAAAGTCAGCAAGAAAGAAAGAAAGCTCCAGAGGCAAG 536

QY 653 CAGGAAAGGGAAGCTTCCCTGTTGAGTTTGCATAGATCCCTAATGAACCTCATACTGC 712
DB 537 CAGGAAAGGGAAGCTTCCCTGTTGAGTTTGCATAGATCCCTAATGAACCTCATACTGC 596
QY 713 TTATGCAACCAAGTGTCTTTATGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATT 772
DB 597 TTATGCAACCAAGTGTCTTTATGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATT 656
QY 773 GAATGGTTTCACTTTTTCATGTGTTCCTTACCTTACTATAAACCAAGGGGAAATGGTATTGC 832
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QY 833 CCAAAAGTCAGGGAGATAATCAGAAAAACAATGGACAAAGTACTCAAAAGACACAAAAAG 892
DB 717 CCAAAAGTCAGGGAGATAATCAGAAAAACAATGGACAAAGTACTCAAAAGACACAAAAAG 776
QY 893 GATAGAAGATCGAGGTAGTAAAGGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATAT 952
DB 777 GATAGAAGATCGAGGTAGTAAAGGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATAT 836
QY 953 AATTGCTTTGCTTTCAGAAAAATGTTTATAGGTAATGCAATAGACTATGCAATAATTTT 1012
DB 837 AATTGCTTTGCTTTCAGAAAAATGTTTATAGGTAATGCAATAGACTATGCAATAATTTT 896
QY 1013 AATCATTAGTATTAAATGGTGTATTAAAGTCTGTGTACTTTG 1054
DB 897 AATCATTAGTATTAAATGGTGTATTAAAGTCTGTGTACTTTG 938
RESULT 10
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LOCUS Homo sapiens BAC clone RP11-367N14 from 4, complete sequence.
DEFINITION AC107214
ACCESSION AC107214.5 GI:23238103
VERSION HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 183317)
Suleston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 183317)
Nguyen, C., Haglund, K. and Spalding, L.
The sequence of Homo sapiens BAC clone RP11-367N14
Unpublished (2001)
JOURNAL 3 (bases 1 to 183317)
Waterston, R.H.
Direct Submission
Submitted (16-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 183317)
Waterston, R.H.
Direct Submission
Submitted (10-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 183317)
Waterston, R.H.
Direct Submission
Submitted (20-SEP-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 183317)
Waterston, R.
Direct Submission
Submitted (03-OCT-2002) Department of Genetics, Washington

REFERENCE
 AUTHORS University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 TITLE 7 (bases 1 to 183317)
 JOURNAL Waterston,R.
 COMMENT Submitted (15-OCT-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Sep 20, 2002 this sequence version replaced gi:20128734.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0367N14

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tatenio,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AC112698.

There is an unresolved tandem repeat from base 87660 to 89441.

Data from AC112698 was used to finish this clone.

FEATURES

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	66. 840
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repeat_region	6690. 6920
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repeat_region	6921. 7263
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repeat_region	7405. 7452
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repeat_region	8141. 8233
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repeat_region	8235. 8583
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repeat_region	8584. 8853
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repeat_region	10696. 10958
repeat_region	/rpt_family="Alu"
repeat_region	10964. 11110
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repeat_region	20263. 20564
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repeat_region	20769. 20995
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repeat_region	21095. 21383

* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 225634: contig of 225634 bp in length
 * 225635 225734: gap of unknown length
 * 225735 231311: contig of 5577 bp in length.

FEATURES

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	end_sequence: BH343917"	
misc_feature	complement(218103..218757)	
	notes="clone_boundary"	
	clone_end:Sp5	
	site:	
	end_sequence: BH343918"	
misc_feature	220260..222134	
	/notes="wgs end extension"	
	clone_end:Sp6"	
misc_feature	222185..225634	
	/notes="wgs end extension"	
	clone_end:Sp6"	
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ORIGIN		
Query Match	63.6%; Score 686.8; DB 2; Length 231311;	
Best Local Similarity	90.5%; Pred. No. 1.3e-136;	
Matches 744; Conservative	0; Mismatches 77; Indels 1; Gaps 1;	
QY	233 TATCAAGAAACGTTAAAGGAAATGATGATGCTACGAAAAATATAGAAGAGATGAT	292
Db	53296 TTTTGTAGAACTTTAAAGGAAATGATGATGCTATGAAAAATATAGAAGAGATGAT	53237
QY	293 TTAACACAGAAAGAGCTTACAGAGCTTCTCCAGAGAGACATAATTAATAGTCAAGAA	352
Db	53236 TCAACACAGAAAGAGCTTACAGAGCTTCTCCAGAGAGACATAATTAATAGTCAAGAA	53177
QY	353 TTGGAGATGAAAAATACAGATGTTACACAAATGCTCGAATTTGTTGGAATTCGGCA	412
Db	53176 TTGGAGATGAAAAATACAGATGTTACACAAATGCTCGAATTTGTTGGAATTCGGCA	53117
QY	413 AGACAAATGAGTTACACTCACAGTGTCTCCAAAGATCTCTGCAAGTGAACGAGCTCA	472
Db	53116 AGACAAATGAGTGTGATTCACAGTGTCTCCAAAGATCTCTGCAAGTGAACGAGCTCA	53057
QY	473 GATAAGCAAGATGAGTTCACGCAACCAAGAAAGATCTTCAAGAGACCCCGAGCAG	532
Db	53056 GACAAATCCAAAGATGATTCAGTCAACCGAAGATCTTCCAGAGACCTCGAAGACAG	52997
QY	533 CGACCAAGTGAAGCCGTGATTTATGTCATCATGCGAAATGGGATGGAAGCTGTGATGAT	592
Db	52996 CGACCAAGTGAAGCCGTGATTTATGTCATCATGCGAAATGGGATGGAAGCTGTGATGAT	52937
QY	593 CAGCCACCTAAAGAAAGAAATCCAAAGTCAAGCAAGAAAGAAAGAAAGCTCCAGGCCAAG	652
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QY	653 CAGAAAGGGAAGCTTCACTGTTGATTTGCAATAGATCCTAATGAACCTACACTATGC	712
Db	52876 CAGGAGAGGGAAGCTTCACTGTTGATTTGCAATAGATCCTAATGAACCTACACTATGC	52817
QY	713 TTATGCAACCAAGTGTCTTATGGGAGATGATAGGATGTGACAAATGACAGTGTCCAAT	772
Db	52816 TTATGTAACCAAGTGTCTTATGGGAGATGATAGGATGTGACAAATGACAGTGTCCAAT	52757

QY	773 GAATGTTTCACTTTTCTGTTTCACTTACCTATAAACCAAGGGGAATCGTATTGC	832
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QY	833 CCNAAGTCAGGGGAGATATAGAAACCAATGACAAAGTACTGAAAGACAAAGAAAG	892
Db	52696 CCNAAGTCAGGGGAGACAGTGAAGAAACCAATGACAAAGTACTGAAAGACAAAGAAAG	52637
QY	893 GATAGAAAGTCCAGGTTAGTAAAGGCCATCCACATTTTAAAGGGTATTCTCTTTTATAT	952
Db	52636 GAGAGAAGCGAGGTAGTGAAGGCCATCC-GGTTTAAAGGGTCTTTGTCTTTATAT	52578
QY	953 AATTCGTTTCTTTCAGAAAAATGTTTTCAGGTAATGCAATGACATGCAATAATTTTT	1012
Db	52577 AATTCGTTTCTTTCAGAAAAATGTTTTCAGGTAATGCAATGACATGCAATAATTTTT	52518
QY	1013 AATCATTAGTATTATGTTGTTTATTAAGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1054
Db	52517 AATCATTAGTATTATGTTGTTTATTAAGTTGTTGTTGTTGTTGTTGTTGTTGTTG	52476
RESULT 14		
AC128348/c		
LOCUS	245104 bp DNA linear HTG 15-NOV-2002	
DEFINITION	Rattus norvegicus clone CH230-129P3, WORKING DRAFT SEQUENCE, 3	
ACCESSION	unordered pieces.	
VERSION	AC128348.3 GI:25007900	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.	
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
	Rattus	
	1 bases 1 to 245104)	
	Muzny,D,Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,	
	Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,	
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	Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hoques,M.,	
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	Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,	
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	Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,	
	Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,	
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Search completed: January 12, 2004, 18:30:25
Job time : 3984 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2004, 19:31:18 ; Search time 281 Seconds
(without alignments)

3460.255 Million cell updates/sec

Title: US-09-513-365A-1

Perfect score: 1481

Sequence: 1 MLGQQQQQLYSSAALLTGER.....DNEKTMDSKSTKTKDRSR 280

Scoring table: BLOSUM62 Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 2276164 seqs, 1736306516 residues

Total number of hits satisfying chosen parameters: 4552328

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA:

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- 2: /cn2.6/prodata/2/pubna/PCT_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

US-10-115-899-6
; Sequence 6, Application US/10115899
; Publication No. US20020151025A1
; GENERAL INFORMATION:
; APPLICANT: Ostuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human ING1L gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/10/115,899
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: human embryonic brain cDNA library
US-10-115-899-6

Alignment Scores:
Pred. No.: 4,03e-159 Length: 840
Score: 1481.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-513-365A-1 (1-280) x US-10-115-899-6 (1-840)

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QY 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40
DB 61 AGCCGGCTGCTACCTGCTACGTCAGGACTACCTTGAGTGGTGGAGTCGCTGCCAC 120

QY 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
DB 121 GACATGCAGAGGAACGTGTCTGTGCTCGAGAGCTGGACAACAATATCAAGAAACGTTA 180

QY 61 LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuGlnLysLys 80
DB 181 AAGGAAATTTGATGATGCTACGAAATAATAAGAAAGAGATGATTTAAACCAAGAGAAA 240

QY 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100
DB 241 CGTCTACAGAGCTTCTCCAGAGAGCCTAATTAATAGTCAGAAATGGAGATGAAA 300

QY 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120
DB 301 ATACAGATTTGTACACAAATGCTCGAATTTGGTGGAAAAATCGGGCAAGACAAATGGAGTTA 360

QY 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
DB 361 CACTCAGTGTTCAGATTCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAGATG 420

QY 141 AspSerGlnProGluArgSerArgArgProArgArgGlnArgThrSerGluSer 160
DB 421 GATTCAGCAACCAAGAAAGATCTTCAGAGACCCCGCAGGCGGCGGACGAGTGAAC 480

QY 161 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGlu 180
DB 481 CGTGATTTATGTCACATGGCAATGGATTTGAAGACTGTGATGATCAGCCACCTAAGAA 540

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DB 541 AAGAAATCCAAGTCAGCAAGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCT 600

QY 201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal 220
DB 601 TCACCTGTTGAGTTTCCAAATAGATCTCTAATGAACCTACATACCTGTTATGCAACCAAGT 660

QY 221 SerTyrGlyGluMetIleGlyCysAspAsnGlnCysProIleGluTrpPheHisPhe 240
DB 661 TCTTATGGGAGATGATAGTGTGACAAATGAACAGTGTCCAATGAATGGTTTCACTTT 720

QY 241 SerCysValSerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGly 260
DB 721 TCATGTGTTTCACTTACCTATAACCAAGGGGAAATGGTATTGCCCAAGTGCAGGGGA 780

QY 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSerArg 280
DB 781 GATAATGAGAAACAATGACAAAGTACTGAAAGACAAAAGGATAGAGATCGAGG 840
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RESULT 2

US-10-115-899-7

; Sequence 7, Application US/10115899

Publication No. US20020151025A1
GENERAL INFORMATION:
APPLICANT: Oetuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
FILE REFERENCE: Q60193
CURRENT APPLICATION NUMBER: US/10/115,899
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/601,478
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JP H10-134679
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: JP H10-73234
PRIOR FILING DATE: 1998-03-05
PRIOR APPLICATION NUMBER: JP H10-38133
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 7
LENGTH: 1078
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human embryonic brain cDNA library
NAME/KEY: CDS
LOCATION: (92)..(931)
US-10-115-899-7

Alignment Scores:
Pred. No.: 5,76e-159 Length: 1078
Score: 1481.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-513-365A-1 (1-280) x US-10-115-899-7 (1-1078)

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DB 152 AGCCGGCTGCTACCTGCTACGTCAGGACTACCTTGAGTGGTGGAGTCGCTGCCAC 211

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DB 212 GACATGCAGAGGAACGTGTCTGTGCTCGAGAGCTGGACAACAATATCAAGAAACGTTA 271

QY 61 LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuGlnLysLys 80
DB 272 AAGGAAATTTGATGATGCTTACGAAATAATAAGAAAGAGATGATTTAAACCAAGAGAAA 331

QY 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100
DB 332 CGTCTACAGAGCTTCTCCAGAGAGCCTAATTAATAGTCAAGAAATGGGAGATGAAAA 391

QY 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120
DB 392 ATACAGATTTGTACACAAATGCTCGAATTTGGTGGAAAAATCGGGCAAGACAAATGGAGTTA 451

QY 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
DB 452 CACTCACAGTGTTCCTCAAGATCTCTGAAAGTGAACGAGCCTCAGATAAGCAAGATG 511

QY 141 AspSerGlnProGluArgSerArgArgProArgArgGlnArgThrSerGluSer 160
DB 512 GATTCAGCAACCAAGAGATCTTCAGAGACCCCGCAGGCGGACGAGTGAAGC 571

QY 161 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGlu 180
DB 572 CGTGATTTATGTCACATGGCAATGGGATTTGAAGACTGTGTGATGATCAGCCACCTAAGAA 631
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;      Number of application data removed - refer to PALM or file wrapper
;      NUMBER OF SEQ ID NOS: 4031
;      SOURCE: NCBI
;      SOFTWARE: Patentin Ver. 2.0
;      SEQ ID NO 3454
;      LENGTH: 8487
;      TYPE: DNA
;      ORGANISM: Homo sapiens
US-09-764-877-3454

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Best Local Similarity:	49.16%	Indels:	10
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DB:	1		

US-09-513-365A-1 (1-280) x US-09-764-877-3454 (1-8487)

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Qy	78	GlnLysLysArgLeuGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnLeuGly	97
Db	6292	CAGAAGCGGCGATGTCGCACTGTGTGCAGCGCGCTGATCCGCACGCCAGAGCTGGGC	6351
Qy	98	AspGluLysIleGlnIleValThrGlnMetLeuLuuValGluAsnArgAlaArgGln	117
Db	6352	GACGAGNAGATCCAGATCTGTAGCCAGATGGTGGAGCTGGTGGAGAACCCGACGCGGCAG	6411
Qy	118	MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArgAlaSerAsp	136
Db	6412	GTGCAAGCCACGTGGAGCTGTTTCGAGCGCAGCAGGAGCTGGCGGACACAGCGGGCAAC	6471
Qy	137	LysAlaLysMetAspSerSerGlnPro-----GluArg	147
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Qy	148	SerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAla	167
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Qy	168	AsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLys	187
Db	6592	CACGACCACGACGCGCGCTCGGGCACACCCCAAGGAGAAAGGCGCAGAGACTCCAAG	6651
Qy	188	LysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle	207
Db	6652	AAGAAGAAGCGCTCCAAAGGCCAAGCGGAGCGAGGCGCTCCCTGTCGCGACCTCCCATC	6711
Qy	208	AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly	227
Db	6712	GACCCCAACGAAACCCAGTACTGCTGTGCAACCCAGGCTCTCTATGGGAGATGATCGGC	6771
Qy	228	CysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyr	247
Db	6772	TGGACAAACGACGATGCCCATCGAGTGGTTCACCTCTCTGTCGCTGGGGCTCAATCAT	6831
Qy	248	LysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp	267
Db	6832	AAACCAAGGGCAAGTGGTACTGTGCCAAGTCCGGGGGAGAACGAGAACCATCGAC	6891
Qy	268	LysSerThrGlnLysThrLysLysAspArg	277
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RESULT 5

US-09-968-653A-2
; Sequence 2, Application US/09968653A
; Publication No. US20030073084A1
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrey V

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> Garkavstev, Igor
> Riabowol, Karl
> TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
> Pathway
>
> NUMBER OF SEQUENCES: 7
> CORRESPONDENCE ADDRESS:
> ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
> STREET: 300 South Wacker Drive
> CITY: Chicago
> STATE: Illinois
> COUNTRY: USA
> ZIP: 60606
>
> COMPUTER READABLE FORM:
> MEDIUM TYPE: Floppy disk
> COMPUTER: IBM PC compatible
> OPERATING SYSTEM: PC-DOS/MS-DOS
> SOFTWARE: PatentIn Release #1.0, Version #1.30
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/09/968,653A
> FILING DATE: 01-Oct-2001
> CLASSIFICATION: <Unknown>
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US/09/006,783A
> FILING DATE: 15-JAN-1998
> ATTORNEY/AGENT INFORMATION:
> NAME: No. US20030073084Ainan, Kevin E
> REGISTRATION NUMBER: 35,303
> REFERENCE/DOCKET NUMBER: 97,837
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 312-913-0001
> TELEFAX: 312-913-0002
> INFORMATION FOR SEQ ID NO: 2:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 2061 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: CDNA
> FEATURE:
> NAME/KEY: CDS
> LOCATION: 16..897
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> US-09-968-653A-2
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> Pred. No.: 4.91e-72 Length: 2061
> Score: 722.00 Matches: 135
> Percent Similarity: 74.36% Conservative: 39
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> Query Match: 48.75% Indels: 14
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> US-09-513-365A-1 (1-280) x US-09-968-653A-2 (1-2061)
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> Qy 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu 95
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> Qy 96 LeuGluAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
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> Db 310 CTGGCGCACCAGAGATCCAGATCGTAGCCAGATGGTGGAGCTGTGAGGAACCGCAGC 369
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> Qy 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
> : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
> Db 370 CGGAGGTGGACACCGACCTGGAGCTGTTTCAGGCGCAGCAGGAGCTGGCGCAGCAGTG 429
>
> Qy 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSer 143
> : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
> Db 430 GGCACACGCGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGGCGTACGCGCAGTCTGAC 489

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QY 144 GlnProGluArgSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
Db 490 AAGCCC-----AACAGCAAGCGCTCAGCGCGGCGCAACCAAGAGAACCGTGAGAAC 543
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspGlnProProLysGluLysLysSer 183
Db 544 GCCTCCAGCAACACAGCAACAGCGCGGCGCTCGGCGCACACCCCAAGGAGAGAGGCC 603
QY 184 LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
Db 604 AAGACTCCAGAGAGAGAGAGCGCTCCAGGCGCAAGCGGAGCGAGAGGGCGTCCCTGCC 663
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 664 GACCTCCCATCGACCCCAAGCAACAGCGAGTACTGTGTGTGCAACAGGTCTCTATGGG 723
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluThrPheHisPheSerCysVal 243
Db 724 GAGATGATCGGCTGCGGACACAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 783
QY 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
Db 784 GGCCTCAATCAATAACCAAGGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 843
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 844 AAGACCATGAGCAAGCCCTGGAGAGAAATCCAAAAAGAGAGG 885

RESULT 6

US-09-968-653A-6

; Sequence 6, Application US/09968653A

; Publication No. US20030073084A1

; GENERAL INFORMATION:

; APPLICANT: Gudkov, Andrey V

; Riabowol, Karl

; Garkavstev, Igor

; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling

; Pathway

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

; STREET: 300 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/968,653A

; FILING DATE: 01-Oct-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/006,783A

; FILING DATE: 15-JAN-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: No. US20030073084Alman, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 97,837

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-913-0001

; TELEFAX: 312-913-0002

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 633 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..630

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-968-653A-6

Alignment Scores:

Pred. No.: 6,28e-66 Length: 633

Score: 662.00 Matches: 125

Percent Similarity: 75.49% Conservative: 29

Best Local Similarity: 61.27% Mismatches: 36

Query Match: 44.70% Indels: 14

DB: 11 Gaps: 2

US-09-513-365A-1 (1-280) x US-09-968-653A-6 (1-633)

QY 86 LeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThr 105
Db 13 GTGCAGCGCGCTGATCCGACCGAGAGCTGGCGGACGAGAGATCCAGATCGTGAGC 72
QY 106 GlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPhe 125
Db 73 CAGATGCTGAGCTGTGTGAGAACCCGACGCGGACAGTGGACAGCCACGTGGAGCTTTC 132
QY 126 GlnAspProAlaGlu-----SerGluArg 133
Db 133 GAGCGCGACAGGAGCTGGCGGACACAGTGGGCAACAGCGGCAAGGTTGGCGGACAGG 192
QY 134 AlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerArgArgProArg 153
Db 193 CCCAATGGCGATGCGGTAGCGAGTCTGACAAAGCCC-----AACAGCAAGCGCTCACGG 246
QY 154 ArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCys 173
Db 247 CGGCGCGCAACACGAGAACCGGTGAGAACCGGCTCAGCAACACCGACCCACGACGCGG 306
QY 174 AspAspGlnProProLysGluLysLysSerLysSerAlaLysLysLysLysArgSerLys 193
Db 307 GCCTCGGCGCACCCCAAGGAGAGAGGCGGCAAGACCTCCCAAGAGAGAGCGCTCCAAG 366
QY 194 AlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGluProThr 213
Db 367 GCCAAGCGGAGCGAGAGCGGTCCCTGCGGACCTCCCATCGACCCCAAGCAACCCACG 426
QY 214 TyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCys 233
Db 427 TACTGTCTGTGCAACAGAGTCTCTATGGGAGATGATCGGCTGCCACACGACGAGTGC 486
QY 234 ProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrp 253
Db 487 CCCATCGAGTGTTCACCTTCTCGTGGGCTCAATCATAAACCAAGGCGCAAGTGG 546
QY 254 TyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGluLysThr 273
Db 547 TACTGTCCCAAGTCCCGGGGAGAGACGAGAGACCATGAGCAACAAAGCCCTGGAGAAATCC 606
QY 274 LysLysAspArg 277
Db 607 AAAAAAGAGAGG 618

RESULT 7

US-09-918-995-37033

; Sequence 37033, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37033
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)-(421)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-37033

Alignment Scores:
Pred. No.: 9,48e-45 Length: 421
Score: 474.00 Matches: 85
Percent Similarity: 90.00% Conservative: 5
Best Local Similarity: 85.00% Mismatches: 10
Query Match: 32.01% Indels: 0
DB: 11 Gaps: 0

US-09-513-365A-1 (1-280) x US-09-918-995-37033 (1-421)

QY 181 LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla 200
Db 3 AAGAATTCCTAGTCAGCAAGAATAAGAACTCTCCGAGGCCACGCAAGGAAGCT 62
QY 201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal 220
Db 63 TCACCTGTTGAGTTTGCAATAGATCCTTAATGAACCTACATACCTTATGCAACCAAGTG 122
QY 221 SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe 240
Db 123 TCTATGGGAGATGATAGATGTCATGAATGAACACCGTCCATTAATGATGGATTCATTT 182
QY 241 SerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGly 260
Db 183 TTATGTGTTTCACTTACCTATTAACCAAGGGGAAATGGTATTGCCACAGTCAAGGGA 242
QY 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSerArg 280
Db 243 GATAATGAGAAAAACAATGGACCAAAAGTACTGATATGACAAAAAACAATAGATCGAGG 302

RESULT 8

US-10-117-722-435
; Sequence 435, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1elel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28CIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 435
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (164)..(1420)
US-10-117-722-435

Alignment Scores:

Pred. No.: 1.03e-30 Length: 1864
Score: 359.00 Matches: 102
Percent Similarity: 34.22% Conservative: 53
Best Local Similarity: 22.52% Mismatches: 100
Query Match: 24.24% Indels: 198
DB: 13 Gaps: 11

US-09-513-365A-1 (1-280) x US-10-117-722-435 (1-1864)

QY 22 ArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHisAsp 41
Db 155 AGGGCGCGGATGTTGTACCTAGAGACTATCTGGAATGATTGAGCAGCTTCTATGGAT 214
QY 42 MetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeuLys 61
Db 215 CTGCGGACCGCTTCACGAAATGCGGAGATGGACCTGCAGGTGCAGATGCAATG--- 271
QY 62 GluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys--- 80
Db 272 -----GATCAACTAGAACAAAGAGTCAGTGAATCTTTATGAATCAAGAAAAAT 322
QY 81 -----ArgLeuGlnGlnLeu-----LeuGlnArgAlaLeuIleAsnSerGln 94
Db 323 AAACCTGAGTGGAGGAGCAATGCAATCCATCAAAAGAGACTACTATAAGCTTTG 382
QY 95 GluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuLeuGluValGluAsnArg 114
Db 383 GAAGATGCGAGTGAAGGTTTCAGTTGGCAACAGATATATGACTTGTGTAGTCACAC 442
QY 115 AlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAla 134
Db 443 TTGAGAAGCTGGATCAGAACTGGCTAAGTTTAAATGGAGCTGGAAGCTGATATGCT 502
QY 134 ----- 134
Db 503 GGAATTACAGAAATATTAGAGAGCGATCTTTTGAATTAGACACTCTTTCACAGCCAGT 562
QY 134 ----- 134
Db 563 AACAATCACCATGCTCATTCACATACTCCAGTGGAAAAAGAAATATAATCAACTTCT 622
QY 134 ----- 134
Db 623 CACCATACGACAAACAGATCATATTCTGAAAAAGAAATTTAAATCTGAAGCTCTTATCC 682
QY 135 -----SerAspLysAlaLys----- 139
Db 683 ACCCTTACGTCAAGTCCCTTAAGGAAAAATACACTAGTTTGCAGAAATAATTAATCCACA 742
QY 140 -----MetAspSerSerGlnPro----- 145
Db 743 GCCTCTTCTAACAATGCCTACAAATGTGAATTCCTCCCACTCTGGGACTCTATAACATT 802
QY 145 ----- 145
Db 803 GGCTGTTATCTTCAGGAACCTGGTCAGGGGCAATTACATGGCAGCTGCTCAAGCAGTT 862
QY 146 GluArgSerSerArgArgProArgGlnArgThrSerGlu----- 159
Db 863 CAGGCTACAGCTCAGATGAGGAGGACCAAGAACATCAAGTTTAAAGCCAGTTATGAA 922
QY 159 ----- 159
Db 923 GCATTTAAGATAATCACTTTTCAGTTGGAAAAAGAAATTTTCAATGGCCAGGAAACAGTT 982
QY 160 -----SerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspGlnPro 177
Db 983 GGCTATTTCATCATCTTCGGCACTTTATGACAAATTAAACACAGATGCCAGTTCATCAGCA 1042
QY 178 ProLysGluLysLysSerLysSerAlaLysLysLysLysLysLysLysLysLysLysLys 197
Db 178 ProLysGluLysLysSerLysSerAlaLysLysLysLysLysLysLysLysLysLysLys 197

198	Qy	ArgGluAla-----	200
		:::	
1103	Db	TCATCTTCCTCCTCCTCTCTCTCCTTATCATCGTGTCTTCTCATCATCAACTGGTGACAA	1162
201	Qy	-----SerProValGluPhe	205
		:::	
1163	Db	GAAATCTCTCAACAACAACATGTAGTGCACGAATCTGATTCAATAGTCAGGTGATTGG	1222
206	Qy	AlaIleAspProAsnGluPurThrTyvCysLeuCysAsnGlnValSerTyvGlyGluMet	225
		:::	
1223	Db	ACTTACGACCCCAATGAACCTCGATACTGCATTGTGTAATCAGGTATCTTATGGTGAGATG	1282
226	Qy	IleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeu	245
		::: :::	
1283	Db	GTGGGATGTGATAACCAAGAATGGCCCTATAGAATGGTTCATTATGCTCGTGTGGATTG	1342
246	Qy	ThrTyrllysProIysGlyIlysTtoTyvCysProIysCys-----Arg	259
1343	Db	ACAGAGCGACCAAAAGGCNAATGGTACTGTCCACAGTCGACTGCTGCAATGAAGAGAGAAGA	1402
260	Qy	GlyAspAsnGluLys-----ThrMetAspLysSerThrGluLysThr	273
1403	Db	GSCAGCAGACACAATAAAGGTGGTCCCTTTTGTGTGATGAAGAAATAAACTTCAGCTGAA	1462
274	Qy	-----LysLysAspArgSerArg	280
1463	Db	GATTTTATATAGGACTTTAAAAAGAGAGAGAGAGAAAGA	1501

```

RESULT 10
US-09-738-973-146
; Sequence 146, Application US/09738973
; Patent No. US20020110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-738-973-146

Alignment Scores:
Pred. No.: 1.82e-26
Score: 314.00
Percent Similarity: 70.29%
Best Local Similarity: 49.28%
Query Match: 21.20%
DB: 10
Matches: 68
Conservative: 29
Mismatches: 31
Indels: 11
Gaps: 2

US-09-513-365A-1 (1-280) x US-09-738-973-146 (1-451)

```

```

Db      77  AAATACCAAGAGATCTTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGCAGACA 136
Qy      75  AspLeuAenGlnIlyLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGln 94
Db      137  GACGGGCGCAGAAAGCGCGGATGCTGCATGTGTGCGAGCGCGCTGATCCGAC-CAG 195
Qy      95  GluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArg 114
Db      196  GAGCTGGCGCAGCAGAGATCCAGATCGTGAGCCAGATGTTGGAGCTGTTGGAGAACCAG 255
Qy      115  AlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArg 133
Db      256  ACGCGGCGAGTGGACACCGCTGCTGAGCGCGCAGCAGGAGTGTGGCGACACA 315
Qy      134  AlaSerAspLysAlaLysMetAspSerSerGlnPro----- 145
Db      316  GCGGGCAACAGCGCAAGCTGGCGCGGACAGGCCAACAGGCGGAGCGCGCAGCGAGCT 375
Qy      146  ---GluArgSerSerArgProArgArgGlnArgThrSerGluSerArgAsp 162
Db      376  GACAAGCCCAACAGCAGCGCTCACGGCGGCGAGCGCAACACGAGAACCGTGAG 429

RESULT 11
US-09-854-133-146
; Sequence 146, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-146

Alignment Scores:
Pred. NO.: 1.82e-26 Length: 451
Score: 314.00 Matches: 68
Percent Similarity: 70.28% Conservative: 29
Best Local Similarity: 49.28% Mismatches: 31
Query Match: 21.20% Indels: 11
DB: 10 Gaps: 2

US-09-513-365A-1 (1-280) x US-09-854-133-146 (1-451)
Qy      35  ValGluSerLeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsn 54
Db      17  ATCCAGTCCCTTCCTTCGACTTCGAGAGAAATGTCCTCGTATCGGGAGATCGACGGG 76
Qy      55  LysTyrGlnGlnThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAsp 74
Db      77  AAATACCAAGAGATCTTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGCAGACA 136
Qy      75  AspLeuAenGlnIlyLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGln 94
Db      137  GACGGGCGCAGAGCGCGGATGCTGCATGTGTGCGAGCGCGCTGATCCGAC-CAG 195
Qy      95  GluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArg 114
Db      196  GAGCTGGCGCAGAGAGATCCAGATCGTGAGCCAGATGTTGGAGCTGTTGGAGAACCAG 255
Qy      115  AlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArg 133

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Db 256 ACAGCGAGGTGGACAGCCAGCTGGAGCTGTCGAGCGCCAGCAGGAGCTGGCGGCACACA 315
Qy 134 AlaSerAspLysAlaLysMetAspSerSerGlnPro----- 145
Db 316 GCGGCAACAGCGGCAAGGCTGGCGGAGACAGCCCAAGGCGGCGCAGCGAGGCT 375
Qy 146 ---GluArgSerSerArgArgProArgGlnArgThrSerGluSerArgAsp 162
Db 376 GACAAGCCCAACAGCAAGCGCTCAGCGGCGCAGCGCAACACAGCAAGACCGTGAG 429

RESULT 12
US-10-144-649A-146
; Sequence 146, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-144-649A-146

Alignment Scores:
Pred. No.: 1,828-26 Length: 451
Score: 314.00 Matches: 68
Percent Similarity: 70.29% Conservative: 29
Best Local Similarity: 49.28% Mismatches: 31
Query Match: 21.20% Indels: 11
DB: 15 Gaps: 2

US-09-513-365A-1 (1-280) x US-10-144-649A-146 (1-451)

Qy 35 ValGluSerLeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsn 54
Db 17 ATCGAGTCCCTGCTTCGACTTGCAGAGAAATGCTCGCTGATCGGAGATCGACGCG 76
Qy 55 LysTyrGlnGluThrLeuLysGluLeuAspValTyrGluLysTyrLysLysGluAsp 74
Db 77 AAATACCAAGAGATCTGAAGAGAGCTAGACGAGTGTCTAGCGGCTTACGTCCGAGACA 136
Qy 75 AspLeuAsnGlnLysLysArgLeuGlnGlnLeuLeuArgAlaLeuLeuLeuSerGln 94
Db 137 GACGGGCGCAGAAAGCGGAGTGTCTGTGTGTCAGCGCGGCTGTATCCGCAC-CAG 195
Qy 95 GluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArg 114
Db 196 GAGCTGGCGCAGAGAAGATCCAGATCGTGAGCCAGATGGTGAGCTGTGTGAGAACCCG 255
Qy 115 AlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArg 133
Db 256 ACAGCGCAGTGGACAGCAGCAGCTGGAGCTGTCGAGCGCAGCAGGAGCTGGCGCACACA 315
Qy 134 AlaSerAspLysAlaLysMetAspSerSerGlnPro----- 145
Db 316 GCGGGCAACAGCGGCAAGGCTGGCGGAGACAGCCCAAGGCGGCGCAGCGAGGCT 375
Qy 146 ---GluArgSerSerArgArgProArgGlnArgThrSerGluSerArgAsp 162
Db 376 GACAAGCCCAACAGCAAGCGCTCAGCGGCGCAGCGCAACACAGCAAGACCGTGAG 429

RESULT 13

US-09-938-842A-1178
; Sequence 1178, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1178
; LENGTH: 813
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1178

Alignment Scores:
Pred. No.: 6,13e-22 Length: 813
Score: 277.50 Matches: 77
Percent Similarity: 45.35% Conservative: 40
Best Local Similarity: 29.84% Mismatches: 81
Query Match: 18.74% Indels: 61
DB: 10 Gaps: 9

US-09-513-365A-1 (1-280) x US-09-938-842A-1178 (1-813)

Qy 27 TyrValGlnAspTyrLeuGluCysValGluSerLeuProHisAspMetGlnArgAsnVal 46
Db 25 TATGTTGATGATTACCTTGAGTATGCAAGCACTTTCCCTGCAGAGCTACAAAGATTACTA 84
Qy 47 SerValLeuArgGluLeuAsp----- 53
Db 85 AACACAGTTTCGGAAGTACAGCAGAGATCTCAATGCTTGTTCACAGAGTTCTAAAAAG 144
Qy 54 -----AsnLysTyrGlnGluThrLeuLysGluLeuAspValTyrGluLysTyr 70
Db 145 GGTATGTTGATGATTCATTAATGTTGTTGATGAGAGAGAGTTTATGCGCCCGCAGCGTATGATCT 204
Qy 71 LysLysGluAspAspLeuAsnGlnLysLysArgLeuGlnGlnLeuGlnArgAlaLeu 90
Db 205 CGTAAAGAGATTGAGTCTAGTCAGGAA----- 231
Qy 91 IleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeu 110
Db 232 ---AATGCTTAAAGTTTGTGTACCGAGAGAGTTTATGCGCCCGCAGCGTATGATCT 288
Qy 111 ValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu 130
Db 289 ATAGATAGTCATGTAAACAGCTTGTATGAAGATCTGAATAATTTT-----GCAGAA 339
Qy 131 SerGluArgAlaSerAspLysAlaLysMetAspSerSerGln----- 144
Db 340 GATTAAAGCAGAGAGGGAATAATCCACAGCAGAGCCCTCTGTTCTTCTCCACCTACCT 399
Qy 145 -----ProGluArgSerSerArgArg-ProArgArgGlnArgThrSerGluSerArgAs 162
Db 400 ATAGTTCTTAAAGCGGAAAGCGTAAGTCTTCTATGGCACACCTCAGCCCAAGAGATT 459
Qy 162 pleuCysHisMetAlaAsnGlyIleGluAspCysAspAspGln-----ProProLysGlu 180
Db 460 GATTATAGAGATAGAGACTGGGATCGT-GACAGGGGATTTTGAGCTCATGCTCTCT 513
Qy 180 uLysLysSerSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAl 200

Db 514-CCAGGAGCAATCGGAAGACCT 536
Qy 200 aserProVal---GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnG1 219
Db 537 TATGCAATTGAAGAGCAGCCCAATCGATCAAAACGAAACCACTTACTGTCTGCCATCA 596
Qy 219 nValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysPro---IleGluTrpPh 238
Db 597 GTGTGCTTTGAGACATGATTTGCTGTGACATGAGAAATTCGAAGGAGGTGAATGGTT 656
Qy 238 ehPheSerCysValSerLeuThrTyrLysPro-----LysGlyLysTrp 253
Db 657 TCACATATACATCGGTGGCTTCACACCTGAGACCAGATTCAAAGGGAAATGG 708

RESULT 14
US-09-801-368-257
; Sequence 257, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Calli, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 257
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-257

Alignment Scores:
Pred. No.: 3,228-20 Length: 993
Score: 263.50 Matches: 75
Percent Similarity: 37.04% Conservative: 45
Best Local Similarity: 23.15% Mismatches: 105
Query Match: 17.79% Indels: 99
DB: 10 Gaps: 8

US-09-513-365A-1 (1-280) x US-09-801-368-257 (1-993)

Qy 28 ValGlnAspTyrLeuGluCysValGluSerLeuProHisAspMetGlnArgAsnValSer 47
Db 31 TTAACGACATACACTGACGTGTGGAGGAATTCCTCCACTGGCCACCTCCAGATATTAAAC 90
Qy 48 ValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeuLysGluLeuAspValTyr 67
Db 91 TTAACACGAAATAGATGCAAAATGTGTGATTCCTATGCGGAATTTGAACGAGAGGATA 150
Qy 68 GluLysTyrLysLysGluAspAsp-----LeuAsn 77
Db 151 GATAAGTTCTTGAAGAAAGACTTCAATAAAGATCAACCAACACAAAGTAAGACTGCTCAAT 210
Qy 78 GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly 97

Db 211 AATATCAACAAGATTATTATGAAGAACTGATGCCATCGCTG----- 249
Qy 98 AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
Db 250 GAGGAGAAATGTCATGTCTCATTCATTATGCTGGTAATATCTAGACAGATTGAGTCCCCGG 309
Qy 118 MetGluLeu----- 120
Db 310 TTAGAATTGGCGTATGAAGTCGCAATCAAGAACACAGAAATCTTAGAGGTTTAAGACTG 369
Qy 121 -----HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAsp 136
Db 370 GGTGTGGACAACCATCCAGCAATGCACCTCCATCATGAACCTAATGAAAAAATAGAGAGC 429
Qy 137 LysAlaLysMetAspSerSerGlnProGluArgSer---SerArgArgPro----- 152
Db 430 AATCAAAACAGCAAAATCGTCGACGCACTGAAGAGCGAATCAAGAGAGCAAGCCATGGCT 489
Qy 153 -----ArgArgGln-----ArgThrSerGluSerArg 161
Db 490 GCCAACAGGAGCGAGCGCAACATTACTCCGCCAGCACACACCAACAGACGACTCAAG 549
Qy 162 AspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLys 181
Db 550 AACGACGCAAACTACGGAGGCGAGCAGGAGCAAGCAACACACTGTAACAACACACA 609
Qy 182 LysSerLys-----SerAlaLysLys 188
Db 610 AACTCAAGAAAAAGAGCCACGCTGCCAATACCAACAGCGCGATCCAGAGACCAAAAA 669
Qy 189 LysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle--- 207
Db 670 CGCAAGAGGAGAGTTGCCACACACGCCGTTTCCACCAAGCACTATCAGCAGCGCAACTGCC 729
Qy 207 ----- 207
Db 730 GTCAATAATGGCAGGATAGGTACATCTACAGCGCTCAGGGGAGTTAGACGCTCGGAAAC 789
Qy 208 -----AspProAsnGluProThrTyrCys 215
Db 790 AGCAACAACAGCAGGATATCAAGACCAAAAAACCAACGACTACGGCGAACCGCTCTACTGC 849
Qy 216 LeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIle 235
Db 850 TACTGTACCAAGTGGCATACGGGGAATGTTGGGGTGTGATGGCGCAGACTGTGAGCTA 909
Qy 236 GluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCys 255
Db 910 GAATGGTTCCATTGTCATGTATTGGACTCGAAACTCTACCTAAGGGCAAGTGGTATTGC 969
Qy 256 ProLysCysArg 259
Db 970 GACGACTGCAAA 981
RESULT 15
US-10-032-585-6348
; Sequence 6348, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6348
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Candida albicans

US-10-032-585-6348

Alignment Scores:

Pred. No.:	4,38e-19	Length:	897
Score:	253.00	Matches:	84
Percent Similarity:	36.25%	Conservative:	36
Best Local Similarity:	25.38%	Mismatches:	108
Query Match:	17.08%	Indels:	104
DB:	13	Gaps:	10

US-09-513-365A-1 (1-280) x US-10-032-585-6348 (1-897)

QY	19	GlulArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeu	38
DB	4	GATACATCACTGTACTTGAGAAATACACACAGGAT-----TTATCTAATCTA	51
QY	39	ProHisAspMetGlnArgValSerValLeuArgGluLeuAspAsnLysTyrGlnGlu	58
DB	52	CCACTTGAGTGAGGCAATTTATTAGAGAAATCAAAAGCAAGATGTACAAGTCTCAGAA	111
QY	59	ThrLeuLys-----GluLeAspAsp	65
DB	112	GCAAGGAACGATACCAAACTCGTGACCATCACTTCATAAATTTATACGAACAAATGGG	171
QY	66	ValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLysArgLeuGlnLeu	85
DB	172	ACACTAACTAAACATCCAAAGGAAGACCACTGTGATTCGAAG-----	213
QY	86	LeuGlnArgAlaLeuLeuAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThr	105
DB	214	ATCGAAGAGATATGAAGCTTGTGCAGAAACTACAGAAAGAGAAATTCATTGGCTAAC	273
QY	106	GlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPhe	125
DB	274	ACTGCATTTGTTTGATATCGAAACATCTATATCATTTTGAG-----	315
QY	126	GlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnPro	145
DB	316	-----ACAGACATTCGCAAGCTAGAAAGAGATGAATT-	347
QY	146	GluArgSerSerArgArgProArgGlnArgThrSer-GluSerArgAspLeuCysHi	165
DB	348	GTTGCCTCTCTTTAGAACACCCCTCGAGCTAACTGAAGTATCTAAAGACGAATACGCAAA	407
QY	165	sMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSe	185
DB	408	ATCACTTAATGGCTTTTCTGATAGTCTCTGCCACACCAACCGCTAGGAATGGATCATC	467
QY	185	rAla-----LysLysLys-----	189
DB	468	GGCACTCCAGTGCAGAAACAGTGAAGAAAGATCCAAAGAGAAACTTAGTGTAAAGG	527
QY	190	-----LysArgSerLysAl	194
DB	528	GGGTCCTCTCTCTCTGCTCAGTCATCTCTGCTTCAAGACAGGTGAAGCGACTCCGGTC	587
QY	194	alysGlnGluArgGluAlaSerProValGlu-----	204
DB	588	AGAAGAGATAGAGGATCCTCTACCGTATGAGGAGGGGTCAATGGCGTTCAATGGAAATGT	647
QY	205	-----PheAlaIleAspProAsnGluProThr-----	213
DB	648	AGCAATCAGCATAAATAGTCAGCAGATGCAAAATGGTCCAAACGGCGAAGATGCTGATAA	707
QY	214	-----TyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnG1	231
DB	708	TAATCTATATGTTTGTCAACGTGTTTCATTTGGTGAATCATGTTGGTTGTGATAATGA	767
QY	231	uGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysG1	251
DB	768	AGACTGTAAGTATGAATGGTTTTCATTTGGAGTTGTTGGGATCACATCACCTCTCAAAGA	827
QY	251	YLys-----TrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSe	269

Db 828 TGACGAAATTTGGTATTGTCTCTGATTGTCT-----TCAAA 863

QY 269 rThrGluLysThrLysLysAspArgSer 279
Db 864 GATGGAGAAAAGAAAAGAAACGGGAAGAAC 894Search completed: January 12, 2004, 19:54:49
Job time : 290 secs

